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FIGURE 238

MMSFLLGAILTLLWAPTAQAEVLLQPDFNAEKFSGLWYVVSMAQDCRVFLGKKDHLSMSTRAI
RPTEEGGLHVHMEFPGADGCNQVDAEYLVKVGSEGHFRVPALGYLDVRIVDTDYSSFAVLYIYK
ELEGALSTMVQLYSRTQDVSPQALKSFQDFYPTLGLPKDMMVMLPQSDACNPESKEAP

Signal peptide:

amino acids 1-20

Tyrosine kinase phosphorylation site.

amino acids 110-117

N-myristoylation sites.

amino acids 7-13, 79-85, 130-136

Amidation site.

amino acids 50-54

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FIGURE 239

GGCGCGCTGGTCCAGGTGAGCGGGCGCGTCCCCGCGACGGCGCTGCCTGCCCCGAGGCGGTTCA
CGTAAAGACAGCGAGATCCTGAGGGCCAGCCGGGAAGGAGGCGTGGATATGGAGCTGGCTGCT
GCCAAGTCCGGGGCCCCGCGCCGCTGCCTAGCGCGTCTGGGGACTCTGTGGGGACGCGCCCCG
CGCCGCGGCTCGGGGACCCGTAGAGCCCGGCGCTGCGCGCATGGCCCTGCTCTCGCGCCCCGC
GCTCACCTCCTGCTCCTCCTCATGGCCGCTGTTGTCAGGTGCCAGGAGCAGGCCAGACCAC
CGACTGGAGAGCCACCCTGAAGACCATCCGGAACGGCGTTCATAAGATAGACACGTACCTGAA
CGCCGCTTGGACCTCCTGGGAGGCGAGGACGGTCTCTGCCAGTATAAATGCAGTGACGGATC
TAAGCCTTTCCCACGTTATGGTTATAAACCTCCCCACCGAATGGATGTGGCTCTCCACTGTT
TGGTGTTCATCTTAACATTGGTATCCCTTCCCTGACAAAGTGTTGCAACCAACACGACAGGTG
CTATGAGACCTGTGGCAAAAGCAAGAATGACTGTGATGAAGAATTCCAGTATTGCCTCTCCAA
GATCTGCCGAGATGTACAGAAAACACTAGGACTAACTCAGCATGTTTCAGGCATGTGAAACAAC
AGTGGAGCTCTTGTTTGACAGTGTTATACATTTAGGTTGTAAACCATATCTGGACAGCCAACG
AGCCGCATGCAGGTGTCATTATGAAGAAAAAACTGATCTTTAAAGGAGATGCCGACAGCTAGT
GACAGATGAAGATGGAAGAACATAACCTTTGACAAATAACTAATGTTTTTACAACATAAACT
GTCTTATTTTTGTGAAAGGATTATTTTGAGACCTTAAATAAATTTATATCTTGATGTTAAAC
CTCAAAGCAAAAAAAGTGAGGGAGATAGTGAGGGGAGGGCACGCTTGTCTTCTCAGGTATCTT
CCCCAGCATTGCTCCCTTACTTAGTATGCCAAATGTCTTGACCAATATCAAAAACAAGTGCTT
GTTTAGCGGAGAATTTTGAAAAGAGGAATATATAACTCAATTTTCACAACCACATTTACCAA
AAAAGAGATCAAATATAAAATTCATCATAATGTCTGTTCAACATTATCTTATTTGGAAAATGG
GGAATTATCACTTACAAGTATTTGTTTACTATGAAATTTTAAATACACATTTATGCCTAGAA
GGAACGGACTTTTTTTTTCTATTTTAATTACACATAATATGTAATTAAAGTACAACATAATAT
GTTGTTTCTCTGTAGCCCGTTGAGCATATGAGTAAGTCACATTTCTATTAGGACTACTTACAA
GGACAAGGTTTCCATTTTCCAGTTGTAAAATTGGAACCATCAGCTGATAACCTCGTAGGGAG
CAACCCAGGATAGCTAAGTGTTATGTAATATGCCTAGAAGGTGATGTGAATGCGATTTCAGAA
GCATAGCCACTCCCATTTTATGAGCTACTCACATGACAAATGTCATCTTTTGCTATAACCTTT
GCCAAGTTAGAGAAAAGATGGATTTAATGAGATAAATGAAAAGATATTTAACCTAAAAAAA
AAAAAAAAAAAAAAAAAAAA

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FIGURE 240

MALLSRPALTLLLLLMAAVVRCQEQAQT TDWRATLKTIRNGVHKIDTYLNAALDLLGGEDGLC
QYKCS DGSKPFPRYGYKPSPPNGCGSPLFGVHLNIGIPSLTKCCNQHDRCYETCGKSKNDCDE
EFQYCLSKICRDVQKTLGLTQHVQACETTVELLFDSVIHLGCKPYLDSQRAACRCHYEETDL

Important features:**Signal peptide:**

amino acids 1-22

N-myristoylation sites:

amino acids 57-63, 93-99

Phospholipase A2 histidine active site:

amino acids 106-114

Neuraxin and MAP1B proteins repeat proteins Block:

amino acids 109-137

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FIGURE 241

GATTCCGAGCGCCTCCACTGCTGGTCCGTTGGCCAGATCAACTCGCCGCGTGGGCCGGCCGTT
CCCTGAGAGTCTGAGCGCTCGCCGCACCCCCTTCCGAGCTTCTATTGGCCGTAGCAGACGTCC
GTCTGCCGCTATCTCCGCCCCAATACGGAAGCGGCCTAGTCCTCCGGCTCCGACAGCTGGGTG
TCCAGGCCATGGGGCAGCCCTGGGCGGCTGGGAGCACGGACGGGGCGCCCGCGCAGCTGCCTC
TCGTGCTCACCGCGCTGTGGGCCGCGGCCGTGGGCCTGGAGCTGGCTTACGTGCTGGTGCTCG
GTCCCGGGCCGCCGCGCTGGGACCCCTGGCCCGGGCCTTGCAGCTGGCGCTGGCCGCCTTCC
AGCTGCTCAACCTGCTGGGCAACGTGGGGCTCTTCCTGCGCTCGGATCCCAGCATCCGTGGCG
TGATGCTGGCCGGCCGCGGTCTGGGCCAGGGCTGGGCTTACTGCTACCAATGCCAAAGCCAGG
TGCCGCCACGCAGCGGACACTGCTCTGCCTGCCGCGTCTGCATCCTGCGTCGGGACCACCACT
GCCGCCTGCTGGGCCGCTGCGTGGGCTTCGGCAACTACCGGCCCTTCCTGTGCCTGCTGCTTC
ATGCCGCCGGCGTCCTGCTCCACGTCTCTGTGCTGCTGGGCCCTGCACTGTCGGCCCTGCTGC
GAGCCACACGCCCCTCCACATGGCTGCCCTCCTCCTGCTTCCCTGGCTCATGTTGCTCACAG
GCAGAGTGTCTCTGGCACAGTTTGCCTTGGCCTTCGTGACGGACACGTGCGTGGCGGGTGCGC
TGCTGTGCGGGGCTGGGCTGCTCTTCCATGGGATGCTGCTGCTGCGGGGCCAGACCACATGGG
AGTGGGCTCGGGGCCAGCACTCCTATGACCTGGGTCCCTGCCACAACCTGCAGGCAGCCCTGG
GGCCCCGCTGGGCCCTCGTCTGGCTCTGGCCCTTCCTGGCCTCCCCATTGCCTGGGGATGGGA
TCACCTTCCAGACCACAGCAGATGTGGGACACACAGCCTCCTGACTCCAGGAAGAGCCAGAGC
TGTGCAGGGAGGAAGGGGTGAGAGGGGGGCCCCACACCTAGACTCAGTAAGGAAGTCGGGTT
GGACCTTAACATCTGCATTGGACAACTCCACCCCTTCCTTGGCCTTGCCCCCTGCCCGCCTACA
CTCCTACGTGTCCAGGGCTTGGGCCGTGACTTAGGCAGAGGAGTGCAGAGGAGGGTCTGGCAG
GGGCTGCTCAGGCCGCTAGCTGCCCCTTTGCCAGGTTAATAAAGCACTGACTTGTTAA

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FIGURE 242

MGQPWAAGSTDGAPAQLPLVLTALWAAVGLLAYVLVLGPGPPPLGPLARALQLALAAFQLL
NLLGNVGLFLRSDPSIRGVMLAGRGLGQGWAYCYQCQSQVPPRSGHCSACRVCILRRDHHCLL
LGRCVGFGNYRPFLCLLLHAAGVLLHVSVLLGPALSALLRAHTPLHMAALLLLPWLMLLTGRV
SLAQFALAFVTDTCVAGALLCGAGLLFHGMILLRGQTTWEWARGQHSYDLGPCHNLQAALGPR
WALVWLWPFLASPLPGDGITFQTTADVGHAS

Important features:**Signal peptide:**

amino acids 1-30

Transmembrane domain:

amino acids 51-66,143-160,174-191,198-214

N-myristoylation sites:

amino acids 2-8,8-14,30-36,81-87,88-94,90-96,206-212

Leucine zipper pattern:

amino acids 143-165,150-172,157-179,164-186

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FIGURE 243

CTTGTCTTTGTGTCGGTTGTGATTTTCCTAATCTCTGATTTTCCTTTTCTCTCGGACGCTCTC
CCTCTTCGGACCCATTTTCTCCCGTGCTTCATGCCCTGATAGCCTGGCCCCCTTCCCGGCTTCC
TTCGCTACCGGGGACGCCTCTAGTTTTTCTGAATTTCTGGCTGGCTCCACCCTCCGCGTTCAT
CTTCCTCAAGAGTTCGCCCCCTCTGGGGGCTCCTCTGTGTAATCGTCGCCTTCTCTGGGTATTT
CTGTGAACTCCGTCTCACACCATCCCGCCATCTTCTCTGCCTTGGCCCCCTTTTCTCTGTACAG
CCAGCTCTGTGTCTTTTCTTCTCCCCCTCTAAAATCGACTCCTCTTCTCCCTGAGAGCCCCA
CCTTTGTGCCCCACTCCTCATTTTCTTACGCCTCCCTCTCTCTGCTGGTCCTCTCTCTCCCTG
CAAGGTTCCATTCCATCAATTTGTTTGTCTTTTGTAGGGGTGGCATCCCCCTCTGACTACTGCT
CCATCCTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTGCTTGAGGATTTCACTTCAATCTTTTCTGGT
TGCGTCTCCACTTGTACTCAGCTTGTTAGGTCCAGGTCCAGTTGTTCTGCATCTGAGGCTGGC
GTGTGCTGTCTTCTCTGATTGGCCTAATCTCCCTCACCCCCGTGAGATCTGTTGTCAGCCTTC
GTTTCTCTTTCCTGTGTCCCAGCTTTTCTGCGGGTCTTGGCACCTTTCTTGGCCACAGATTTT
TGGGTTACAGAGCATGTGTGTCTGAGGCATTGCAGGCAGAAAAGGGTGGCCGACGTGACCTCT
AGCTGGACTGCTGGGCAGGGGAGCTGTCCTAGATAAAAATTGGAAAGAAACAGTGACCCAGAGA
CAGGTGGACAAAGAATTCGGGGACTGATGGGAACTGAGCTTGGGATCCAGACTGAAACTGATT
CCAGACTGACCTCTAGCACCCAGGACCCAGACACAGGGGCC**ATG**GGGACCCCAGCATTTGAGACT
TGTGCAGCTGTTCTGCCTTCTAGGGGCCATCCCCACTCTGCCTCGGGCTGGAGCTCTTTTGTG
CTATGAAGCAACAGCCTCAAGATTCAGAGCTGTTGCTTTCCATAACTGGAAGTGGCTTCTGAT
GAGGAACATGGTGTGTAAGCTGCAAGAGGGCTGCGAGGAGACGCTAGTGTTTCATTGAGACAGG
GACTGCAAGGGGAGTTGTGGGCTTTAAAGGCTGCAGCTCGTCTTCGTCTTACCCTGCGCAAAT
CTCCTACCTTGTTTCCCCACCCGAGTGTCCATTGCCTCCTACAGTCGCGTCTGCCGGTCTTA
TCTCTGCAACAACCTCACCAATTTGGAGCCTTTTGTGAAACTCAAGGCCAGCACTCCTAAGTC
TATCACATCTGCGTCCTGTAGCTGCCCCGACCTGTGTGGGCGAGCACATGAAGGATTGCCTCCC
AAATTTTGTCAACCACTAATTCTTGCCCCCTTGGCTGCTTCTACGTGTTACAGTTCCACCTTAAA
ATTTTCAGGCAGGGTTTCTCAATACCACCTTCCTCCTCATGGGGTGTGCTCGTGAACATAACCA
GCTTTTAGCAGATTTTCATCATATTGGGAGCATCAAAGTGACTGAGGTCTCAACATCTTAGA
GAAGTCTCAGATTGTTGGTGCAGCATCCTCCAGGCAAGATCCTGCTTGGGGTGTGCTCTTAGG
CCTCCTGTTTGCCTTCAGGGAC**TGA**CCATCTAGCTGCACCCGACAAGCACCCAGACTCTTTCA
CATAACAAATAAAATAGCAGAGTTCCTTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
AAAAAAAAA

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FIGURE 244

MGPQHRLRLVQLFCLLGAIPTLPRAGALLCYEATASRFRAVAFHNWKWLLMRNMVCKLQEGCEE
TLVFIETGTARGVVGFKGCSSSSSYPAQISYLVSPPGVSIASYSRVCRSYLCNNLTNLEPFVK
LKA STPKSITSASCSCPTCVGEHMKDCLPNFVTTNSCPLAASTCYSSTLKFQAGFLNTTFLLM
GCAREHNQLLADFH HIGSIKVTEVLNILEKSQIVGAASSRQDPAWGVVLGLLFAFRD

Important features:**Signal peptide:**

amino acids 1-20

N-glycosylation sites:

amino acids 117-121, 183-187

N-myristoylation sites:amino acids 16-22, 25-31, 60-66, 71-77, 81-87, 100-106, 224-230,
235-241, 239-245**Prokaryotic membrane lipoprotein lipid attachment site:**

amino acids 181-192

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FIGURE 245

GTGGAGTTGGGTGGTGTCTGGGAGCCTCTCCCTGAGGGGCACCGCGTCTTCAGGAGCTGGGCCTCCAGTGCGGGCGC
GATGTCAGGCGCGGTGACAGCTCTGTGAGTCCGAGGCCGCGGCCGTGGCGCTGGGCGGCTGCGGGGCCTGACCGG
TCCGCTCCATGGTGCCGCCACGACGCCATCGCGGGCAGGAAGGCCAGGGGTGCTGAGTTCTTCACCTCCTTTTAG
ACTGAGATCTGCCAAGTTTTCCGGCATTGCTCTTGAGGATCTCAGAAGGGCTCTTAAGACAAGACTGCAAATGGT
GTGTGTATTTGTTCATGAACCGAATGAATTTCCAGAACAGTGGTTTCACCTCAGCGCAGGCGAATGGCTCTTGGGAT
TGTTATTCTTCTGCTTGTTGATGTGATATGGGTTGCTTCCTCTGAACCTACTTCGTATGTTTTTACCCAGTACAA
CAAACCATTCTTCAGCACCTTTGCAAAAACATCTATGTTTGTGTTTGTACCTTTGGGCTTTATTATTTGGAAGCC
ATGGAGACAACAGTGTACAAGAGGACTTCGCGGAAAGCATGCTGCTTTTTTTGCGAGATGCTGAAGGTTACTTTGC
TGCTTGCACAACAGATACAACATGAATAGTTCTTTGAGTGAACCTCTGTATGTGCCTGTGAAATTCCATGATCT
TCCAAGTAAAAACCTGAGAGCACAAACATTGATACTGAAAAAACCCCAAAAAGTCTCGTGTGAGGTTTCAGTAA
TATCATGGAGATTGACAGCTTCCGTCAAGTCATGCATTGGAAGCAAAGTTGTCTCGCATGTCATATCCTGTGAA
AGAACAAGAATCCATACTGAAAACGTGGGGAAACTTACTGCAACTCAAGTAGCGAAAATTAGCTTTTTTTTTTTG
CTTTGTGTGGTTTTTTGGCAAATTTGTTCATATCAAGAAGCACTTTCAGACACACAAGTTGCTATAGTTAATATTTT
ATCTTCAACTTCCGGACTTTTTACCTTAATCCTTGCTGCAGTATTTCCAAGTAACAGTGGAGATAGATTTACCCT
TTCTAAACTATTAGCTGTAATTTTAAGCATTGGAGGCGTTGTACTGGTAAACCTGGCAGGGTCTGAAAAACCTGC
TGGAAGAGACACAGTAGGTTCCATTTGGTCTCTTGCTGGAGCCATGCTCTATGCTGTCTATATTGTTATGATTAA
GAGAAAAGTAGATAGAGAAGACAAGTTGGATATTCCAATGTTCTTTGGTTTTGTAGGTTTGTGTTAATCTGCTGCT
CTTATGGCCAGGTTTCTTTTTACTTCATTATACTGGATTTGAGGACTTCGAGTTTCCCAATAAAGTAGTATTAAT
GTGCATTATCATTAATGGCCTTATTGGAACAGTACTCTCAGAGTTCCGTGTGGTTGTGGGGCTGCTTTCTTACCTC
ATCATTGATAGGCACACTTGCACTAAGCCTTACAATACCTCTGTCCATAATAGCTGACATGTGTATGCAAAAGGT
GCAGTTTTCTTGTTATTTTTTGCAGGAGCTATCCCTGTATTTTTTTTCATTTTTTATTGTAACCTCTCCTATGCCA
TTATAATAATTGGGATCCTGTGATGGTGGGAATCAGAAGAATATTTGCTTTTATATGCAGAAAACATCGAATTCA
GAGAGTTCCAGAAGACAGCGAACAGTGTGAGAGTCTCATTTCTATGCACAGTGTTCCTCAGGAGGATGGAGCTAG
TTAGCTGTCTGTTGTCTGTAGCCCAGCTTGATAATGGAACCTATACAGCGAAGAGACAATCTCTGGCAAGTTTTTG
TAGAAAAAATGTTTCAGTGCCTAGTCTGAAAAATAACAGTTTGAGTTCTTTGAAACTCTAAAATATATTTTTCTC
ATACCTGTTTTCTTCATTTTCATAATGAAGCACTTTGCTATGTAGCTGTGTACATATCACTACAGTTATAGGAAG
TTTCAGTCTACAGTCCATCCAAAGGACCAACCTGCCTTACACATCTCAAGGAATTCAGCTGTTGAAATCATTTGA
ACTAATCAAGGAATAAATCCTAATGTTCTGGGACTTTATTTTCACATGTTAAATGCTGGAATATATTATGAAAAT
GTTTTCAAGAAATCACTTAAGTGTTTCATAGACCAGTATTTCTGACAGGTAAATGCTAAAATAAGCTACCTGTAA
TAAGTGTGGATTATATTTTTGGGTTTTGTAGAATATTGCAAAATTAACCACACAAAAAATGTTTAATTTATGCAAC
AAGCATGTTTGTGCAAATTTTCATGGGACTTTAAAAAGAATAAGTATTTGAGAAAATATCTGGTTCACTTACACTA
CATTTACTGTATTATTCTTTTATAGCATTAGGTGCCTTGATTTTAAATCTGTGACAAACCATGGCAAATTTTTTA
AAGGGGAAGTATTATTATAAAATGAAGAAATATGTATTTCTAAAGGCTATATTGCTGTAAACTTAATTGATAAAG
CTCTGTTTAATTTAGAGTTTTGAAGAAATAGTCTCCCTTCAATTAAGAAATTTTCATAATGGAATGATTTAAATT
GAAGTGACAAAGAGTATTATTAAATACAATGTTTATAAAAAAA

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FIGURE 246

MVPPRRHRGAGRPGVLSSSPFRLRSAKFSGIALEDLRRALKTRLQMVCFVMNRMNSQNSGF
TQRRRMALGIVILLVLDVIWVASSELTSYVFTQYNKPFFSTFAKTSMFVLYLLGFIIWKPWRQ
QCTRGLRGKHAAFFADAEGYFAACTTDTTMNSSLSEPLYVPVKFHDLPSEKPESTNIDTEKTP
KKSRRVRFNIMEIRQLPSSHALEAKLSRMSYPVKEQESILKTVGKLTATQVAKISFFFCFVWF
LANLSYQEALSDTQVAIVNILSSTSGLFLLILAAVFPSNSGDRFTLSKLLAVILSIGGVVLVN
LAGSEKPAGRDTVGSISLAGAMLYAVYIVMIKRKVDREDKLDIPMFFGFVGLFNLLLLWPGF
FLLHYTGFEDEFEPNKVVLMCIIINGLIGTVLSEFLWLWGCFLTSSLIGTLALSLTIPLSIIA
DMCMQKVQFSWLFFAGAI PVFFSFFIVTLLCHYNNWDPVMVGIRRIFAFICRKHRIQRPEDS
EQCESLISMHSVSQEDGAS

Important features:**Transmembrane domain:**

amino acids 69-87, 105-118, 237-256, 266-285, 300-316, 332-346,
364-379, 399-419, 453-472

N-glycosylation sites:

amino acids 157-161, 255-259

N-myristoylation sites:

amino acids 14-20, 329-335, 404-410, 407-413, 418-424

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FIGURE 247

CGTCTGTAGAGATATCATGAACTTCAACTTAGCTTTGGTACTTTCTTCCCTGAAGACAGAGGG
CAGAACTCTGAGTTCCAGAACCATTTTCAACTGTATTGGGGACCAATCACTTGACTCTATTCT
TGTCTCTCTGACAGATGACGCTACACTCTCCTCTGAATAATGGACACCATTTCTAAACTGAA
TCCTGCTACTAAAATAATTGAGATGATATATTTTTCCAATTCTACAATCTTGCTTTGTTTTAT
TTAGTTGTTTTCTCTCTCTCTTCCCAGTTTTCCAGAGACTGGAGCTAAACTGGGCTTTCAACA
TCATC**ATGA**AGTTTATCCTCCTCTGGGCCCTCTTGAATCTGACTGTTGCTTTGGCCTTTAATC
CAGATTACACAGTCAGCTCCACTCCCCCTTACTTGGTCTATTTGAAATCTGACTACTTGCCCT
GCGCTGGAGTCCTGATCCACCCGCTTTGGGTGATCACAGCTGCACACTGCAATTTACCAAAGC
TTCGGGTGATATTGGGGGTTACAATCCCAGCAGACTCTAATGAAAAGCATCTGCAAGTGATTG
GCTATGAGAAGATGATTCATCATCCACACTTCTCAGTCACTTCTATTGATCATGACATCATGC
TAATCAAGCTGAAAACAGAGGCTGAACTCAATGACTATGTGAAATTAGCCAACCTGCCCTACC
AACTATCTCTGAAAATACCATGTGCTCTGTCTCTACCTGGAGCTACAATGTGTGTGATATCT
ACAAAGAGCCCGATTCACTGCAAACGTGAACATCTCTGTAATCTCCAAGCCTCAGTGTGCGG
ATGCCTATAAAACCTACAACATCACGGAAAATATGCTGTGTGTGGGCATTGTGCCAGGAAGGA
GGCAGCCCTGCAAGGAAGTTTCTGCTGCCCCGGCAATCTGCAATGGGATGCTTCAAGGAATCC
TGTCTTTTGCGGATGGATGTGTTTTGAGAGCCGATGTTGGCATCTATGCCAAAATTTTTTACT
ATATACCCTGGATTGAAAATGTAATCCAAAATAACT**TGA**GCTGTGGCAGTTGTGGACCATATGA
CACAGCTTGTCCCCATCGTTCACCTTTAGAATTAAATATAAATTAACCTCCTC

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FIGURE 248

MKFILLWALLNLTVALAFNPDYTVSSTPPYLVYLKSDYLPAGVLIHPLWVITAAHCNLPKLR
VILGVTIPADSNEKHLQVIGYEKMIHHPHFSVTSIDHDIMLIKTKTEAELNDYVKLANLPYQT
ISENTMCSVSTWSYNVCDIYKEPDSLQTVNISVISKPQCRDAYKTYNITENMLCVGIVPGRRQ
PCKEVSAAPAICNGMLQGILSFADGCVLRADVGIYAKIFYYPWIENVIQNN

Important features:**Signal peptide:**

amino acids 1-17

N-glycosylation sites:

amino acids 11-15, 156-160, 173-177

Tyrosine kinase phosphorylation site:

amino acids 108-117

N-myristoylation sites:

amino acids 182-188, 203-209

Amidation site:

amino acids 185-189

Serine proteases, trypsin family, histidine active site:

amino acids 52-58

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FIGURE 249

GCGAGGCGGCCGCTGTCTTCTGCTGCGGCTTCCGCGACCACAAGTACTGCTGCGACGACCCGC
ACAGCTTCTTCCCCTACGAGCACAGCTACATGTGGTGGCTCAGCATTGGCGCTCTCATAGGCC
TGTCCGTAGCAGCAGTGGTTCTTCTCGCCTTCATTGTTACCGCCTGTGTGCTCTGCTACCTGT
TCATCAGCTCTAAGCCCCACACAAAGTTGGACCTGGGCTTGAGCTTACAGACAGCAGGCCCTG
AGGAGGTTTCTCCTGACTGCCAAGGTGTGAACACAGGCATGGCGGCAGAAGTGCCAAAAGTGA
GCCCTCTCCAGCAGAGTTACTCCTGCTTGAACCCGCAGCTGGAGAGCAATGAGGGGCAGGCTG
TGAACTCCAAACGCCTCCTCCATCATTGCTTCATGGCCACAGTGACCACCAGTGACATTCCAG
GCAGCCCTGAGGAAGCCTCTGTACCCAACCCTGACCTATGTGGACCAGTCCCATAAACATTCA
ATAAATGTCTCCATACCATCAA

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FIGURE 250

MWWLSIGALIGLSVAADVLLAFIVTACVLCYLFISSKPHTKLDLGLSLQTAGPEEVSPDCQGV
NTGMAAEVPKVSPLQQSYSCLNPQLESNEGQAVNSKRLLHHC FMATVTTSDIPGSPEEASVPN
PDL CGPVP

Important features:

Signal peptide:

Amino acids 1-26

N-myristoylation sites:

Amino acids 7-13, 11-17, 62-68, 93-99

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FIGURE 251

GTGGTTTGGATTGAGCCGGGCCCCGGCCGGGGCGCCGAGTCGGAGGGGGTGGCAGTGAGCGGCG
GCAGAGGCTACGGGGCTCGGTTTGGCTGACTGGGGAGTCGGCAGGCGGCAGGAACC**ATG**CGAG
GCCAGCGGAGCCTGCTGCTGGGCCCCGGCCCGCCTCTGCCTCCGCCTCCTTCTGCTGCTGGGT
ACAGGCGCCGCTGTCCACCTCTACTCCGGGGTCTAGTACAGCGCTGGCGCTACGGCAAGGTCT
GCCTGCGCTCCCTGCTCTACAACCTCCTTTGGGGGCAGTGACACCGCTGTTGATGCTGCCTTTG
AGCCTGTCTACTGGCTGGTAGACAACGTGATCCGCTGGTTTGGAGTGGTGTTTCGTGGTCCTGG
TGATCGTGCTGACAGGCTCCATTGTAGCTATCGCCTACCTGTGTGTCCTGCCTCTCATCCTCC
GAACCTACTCAGTGCCACGACTCTGCTGGCATTCTTCTATAGCCACTGGAATCTGATCCTGA
TTGTCTTCCACTACTACCAGGCCATCACCCTCCGCTGGGTACCCACCCAGGGCAGGAATG
ATATCGCCACCGTCTCCATCTGTAAGAAGTGCATTTACCCCAAGCCAGCCCGAACACACCACT
GCAGCATCTGCAACAGGTGTGTGCTGAAGATGGATCACCCTGCCCCTGGCTAAACAATTGTG
TGGGCCACTATAACCATCGGTACTTCTTCTCTTTCTGCTTTTTTCATGACTCTGGGCTGTGTCT
ACTGCAGCTATGGAAGTTGGGACCTTTTCCGGGAGGCTTATGCTGCCATTGAGACTTATCACC
AGACCCACCCACCCACCTTCTCCTTTTCGAGAAAGGATGACTCACAAGAGTCTTGTCTACCTCT
GGTTCCTGTGCAGTTCTGTGGCACTTGCCCTGGGTGCCCTAACTGTATGGCATGCTGTTCTCA
TCAGTCGAGGTGAGACTAGCATCGAAAGGCACATCAACAAGAAGGAGAGACGTCGGCTACAGG
CCAAGGGCAGAGTATTTAGGAATCCTTACAACCTACGGCTGCTTGGACAACCTGGAAGGTATTCC
TGGGTGTGGATACAGGAAGGCACTGGCTTACTCGGGTGCTCTTACCTTCTAGTCACTTGCCCC
ATGGGAATGGAATGAGCTGGGAGCCCCCTCCCTGGGTGACTGCTCACTCAGCCTCTGTGATGG
CAGTG**TGAG**CTGGACTGTGTGTCAGCCACGACTCGAGCACTCATTCTGCTCCCTATGTTATTTCA
AGGGCCTCCAAGGGCAGCTTTTCTCAGAATCCTTGATCAAAAAGAGCCAGTGGGCCTGCCTTA
GGGTACCATGCAGGACAATTCAAGGACCAGCCTTTTTTACCACTGCAGAAGAAAGACACAATGT
GGAGAAATCTTAGGACTGACATCCCTTTACTCAGGCAAACAGAAGTTCCAACCCCACTAGG
GGTCAGGCAGCTAGCTACCTACCTTGCCCAGTGCTGACCCGGACCTCCTCCAGGATACAGCAC
TGAGATTGGCCACCACCTCTTCTACTTGCTGTCTGAAAAAACACCTGACTAGTACAGCTGAGA
TCTTGGCTTCTCAACAGGGCAAAGATAACCAGGCCTGCTGCTGAGGTCACTGCCACTTCTCACA
TGCTGCTTAAGGGAGCACAAATAAAGGTATTTCGATTTTTTAAAAAAAAAAAAAAAAAAAAAA
AAAAAAAAAAAAA

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FIGURE 252

MRGQRSLLLGPARLCLRLLLLLLGYRRRCPLLRLGLVQRWRYGKVCLRSLLYNSFGGSDTAVDA
AFEPVYWLVDNVIRWFGVVVFVVLVIVLTGSIVAIAYLCVLPLILRTYSVPRLCWHFFYSHWNL
ILIVFHYYQAITTPPGYPPQGRNDIATVSICKKCIYPKPARTHHCSICNRCVLKMDHHCPWLN
NCVGHYNHRYFFSFCFFMTLGCVCYSYGSWDLFREAYAAIETYHQTPPPTFSFRERMTHKSLV
YLWFLCSSVALALGALTVWHAVLISRGETSIERHINKKERRRLQAKGRVFRNPYNYGCLDNWK
VFLGVDTGRHWLTRVLLPSSHLPHGNGMSWEPPPWVTAHSASVMAV

Important features:**Transmembrane domain:**

amino acids 88-100,202-216,254-274

N-myristoylation sites:

amino acids 55-61,56-62,92-98,210-216,309-315,319-325,340-346

Prokaryotic membrane lipoprotein lipid attachment site:

amino acids 201-212

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FIGURE 253

GATCAAGCGCCTTCCTTTCCCTTCCTCTCCCTACTTGGCCTTTGCCCTAAGCCAAGACCTGGCCATCAGCCTGGC
TGCAGGGGCCTGCAGAGCCAGCTGCACCTTTTTCAGGTATGGGGGAGGGCCAGGCACCATGAAGCCAGTGTGGGTG
GCCACCCTTCTGTGGATGCTACTGCTGGTGCCAGGCTGGGGGCCGCCCGGAAGGGGTCCCCAGAAGAGGCCTCC
TTCTACTATGGAACCTTCCCTCTTGGCTTCTCCTGGGGCGTGGGCAGTTCTGCCTACCAGACGGAGGGCGCCTGG
GACCAGGACGGGAAAGGGCCTAGCATCTGGGACGTCTTCACACACAGTGGGAAGGGGAAAGTGCTTGGGAATGAG
ACGGCAGATGTAGCCTGTGACGGCTACTACAAGGTCCAGGAGGACATCATTCTGCTGAGGGAAGTGCACGTCAAC
CACTACCGATTCTCCCTGTCTTGGCCCCGGCTCCTGCCACAGGCATCCGAGCCGAGCAGGTGAACAAGAAGGGA
ATCGAATTCTACAGTGATCTTATCGATGCCCTTCTGAGCAGCAACATCACTCCCATCGTGACCTTGCACCACTGG
GATCTGCCACAGCTGCTCCAGGTCAAATACGGTGGGTGGCAGAATGTGAGCATGGCCAACTACTTCAGAGACTAC
GCCAACCTGTGCTTTGAGGCCTTTGGGGACCGTGTGAAGCACTGGATCACGTTTCAGTGATCCTCGGGCAATGGCA
GAAAAAGGCTATGAGACGGGCCACCATGCGCCGGGCCTGAAGCTCCGCGGCACCGGCCTGTACAAGGCAGCACAC
CACATCATTAAGGCCACGCCAAAACCTGGCATTCTTATAACACCACGTGGCGCAGCAAGCAGCAAGGTCTGGTG
GGAATTTCACTGAACTGTGACTGGGGGGAACCTGTGGACATTAGTAACCCCAAGGACCTAGAGGCTGCCGAGAGA
TACCTACAGTTCTGTCTGGGCTGGTTTGCCAACCCCATTTATGCCGGTGACTACCCCAAGTCATGAAGGACTAC
ATTGGAAGAAAGAGTGCAGAGCAAGGCCTGGAGATGTGAGGTTACCGGTGTTCTCACTCCAGGAGAAGAGCTAC
ATTAAAGGCACATCCGATTTCTTGGGATTAGGTCAATTTTACTACTCGGTACATCACGGAAGGAACTACCCCTCC
CGCCAGGGGGCCAGCTACCAGAACGATCGTGACTTGATAGAGCTGGTTGACCCAACTGGCCAGATCTGGGGTCT
AAATGGCTATATTCTGTGCCATGGGGATTTAGGAGGCTCCTTAACTTTGCTCAGACTCAATACGGTGATCCTCCC
ATATATGTGATGGAAAATGGAGCATCTCAAAAATTCCACTGTACTCAATTATGTGATGAGTGGAGAATTCAATAC
CTTAAAGGATACATAAATGAAATGCTAAAAGCTATAAAAGATGGTGCTAATATAAAGGGGTATACTTCCTGGTCT
CTGTTGGATAAGTTTGAATGGGAGAAAGGATACTCAGATAGATATGGATTCTACTATGTTGAATTTAACGACAGA
AATAAGCCTCGCTATCCAAAGGCTTCAGTTCAATATTACAAGAAGATTATCATTGCCAATGGGTTTCCCAATCCA
AGAGAGGTGGAAAGTTGGTACCTCAAAGCTTTGGAACTTGCTCTATCAACAATCAGATGCTTGCTGCAGAGCCT
TTGCTAAGTCACATGCAAATGGTTACGGAGATCGTGGTACCCACTGTCTGCTCCCTCTGTGTCCTCATCACTGCT
GTTCTACTAATGCTCCTCCTGAGGAGGCAGAGCTTGAGACAGGATTATCAATTTTGGAGCTTCATAAGAGAATCTT
CAGGATCTTCCTCCCTTTTCTGCTTTGAGGGTTTCCATACATTGCTGTTTTTCAGGTTCTACAATAATTACCTTTT
TTTCTCTTTCTCTTTTGGCTTGTGCTGGGATTTAAGAATTAGAAAATAAAAATAAGCAGAAATTA

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FIGURE 254

MKPVVWVATLLWMLLLVPRLLGAARKGSPEEASFYYGTFPLGFSWGVGSSAYQTEGAWDQDGKGPSIWDVFTHSKGK
KVLGNETADVACDGYIKVQEDIILLRELHVNHYRFSLSWPRLPTGIRAEQVNKKGIEFYSDLIDALLSSNITPI
VTLHHWDLPLQLQVKYGGWQNVSMANYFRDYANLCFEAFGDRVKHWITFSDPRAMAEKGYETGHHAPGLKLRGTG
LYKAAHHIIKAHAKTWHSYNTTWRSKQQGLVGISLNCDWGEPVDISNPKDLEAAERYLQFCLGWGFANPIYAGDYP
QVMKDYIGRKSAEQGLEMSRLPVFSLQEKSYIKGTSDFLGLGHFTTRYITERNYPSRQGSPSYQNDRLIELVDPN
WPDLGSKWLYSVPWGFRRLLNFAQTQYGDPIIYVMENGASQKFHCTQLCDEWRIQYLKGYINEMLKAIKDGANIK
GYTSWSLLDKFEWEKGYSRDYGFYYVEFNDRNKPRYPKASVQYYKKIIANGFPNPREVESWYLKALETCSINNQ
MLAAEPLLSHMQMVTIVPTVCSLCVLITAVLLMMLLLRRQS

Important features:**Signal peptide:**

amino acids 1-21

Transmembrane domain:

amino acids 541-558

N-glycosylation sites:

amino acids 80-84,171-175,245-249

Glycosaminoglycan attachment site:

amino acids 72-76

cAMP- and cGMP-dependent protein kinase phosphorylation sites:

amino acids 23-27,564-568

Tyrosine kinase phosphorylation sites:

amino acids 203-211,347-355,460-468,507-514

N-myristoylation sites:

amino acids 44-50,79-85,167-173,225-231,257-263,315-321

Amidation site:

amino acids 307-311

Glycosyl hydrolases family 1 active site:

amino acids 407-416

Glycosyl hydrolases family 1 N-terminal signature:

amino acids 41-56

Motif name Glycosyl hydrolases family:

amino acids 37- 67

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FIGURE 255

CGCGAAG**ATG**CGAAAGGTGGTTTTGATCACCGGGGCTAGCAGTGGCATTGGCCTGGCCCTCTG
CAAGCGGCTGCTGGCGGAAGATGATGAGCTTCATCTGTGTTTGGCGTGCAGGAACATGAGCAA
GGCAGAAGCTGTCTGTGCTGCTCTGCTGGCCTCTCACCCCACTGCTGAGGTCAACCATTGTCCA
GGTGGATGTCAGCAACCTGCAGTCGGTCTTCCGGGCCTCCAAGGAACCTTAAGCAAAGGTTTCA
GAGATTAGACTGTATATATCTAAATGCTGGGATCATGCCTAATCCACAACCTAAATATCAAAGC
ACTTTTCTTTGGCCTCTTTTCAAGAAAAGTGATTCATATGTTCTCCACAGCTGAAGGCCTGCT
GACCCAGGGTGATAAGATCACTGCTGATGGACTTCAGGAGGTGTTTGAGACCAATGTCTTTGG
CCATTTTATCCTGATTCGGGAACCTGGAGCCTCTCCTCTGTCACAGTGACAATCCATCTCAGCT
CATCTGGACATCATCTCGCAGTGCAAGGAAATCTAATTTTCAGCCTCGAGGACTTCCAGCACAG
CAAAGGCAAGGAACCCTACAGCTCTTCCAAATATGCCACTGACCTTTTGAGTGTGGCTTTGAA
CAGGAACTTCAACCAGCAGGGTCTCTATTCCAATGTGGCCTGTCCAGGTACAGCATTGACCAA
TTTGACATATGGAATTCTGCCTCCGTTTATATGGACGCTGTTGATGCCGGCAATATTGCTACT
TCGCTTTTTTTGCAAATGCATTCACTTTGACACCATATAATGGAACAGAAGCTCTGGTATGGCT
TTTCCACCAAAGCCTGAATCTCTCAATCCTCTGATCAAATATCTGAGTGCCACCACTGGCTT
TGGAAGAAATTATATTATGACCCAGAAGATGGACCTAGATGAAGACACTGCTGAAAAATTTTA
TCAAAAGTTACTGGAACCTGGAAAAGCACATTAGGGTCACTATTCAAAAAACAGATAATCAGGC
CAGGCTCAGTGGCTCATGCCTA**TAA**ATTCCAGCACTTTGGGAGGCCAAGGCAGAAGGATCACTT
GAGACCAGGAGTTCAAGACCAGCCTGAGAAACATAGTGAGCCCTTGTCTCTACAAAAGAAAT
AAAAATAATAGCTGGGTGTGGTGGCATGCGCATGTAGTCCCAGCTACTCAGAAGGATGAGGTG
GGAGGATCTCTTGAGGCTGGGAGGCAGAGGTTGCAGTGAGCTGAGATTGTGCCACTGCACTCC
AGCCTGGGTGACAGCGAGACCCTGTCTCAAATATGTATATATTTAATATATATATAAAACCA
GAGCTGACAATGACACTCTGGAACATTGCATACCTTCTGTACATTCTGGGGTACATGGATTTC
TACTGAGTTGGATAATATGCATTTGTAATAAACTATGAACTATGAA

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FIGURE 256

MRKVVLITGASSGIGLALCKRLLAEDDELHLCLACRNMSKAEAVCAALLASHPTAEVTIVQVD
VSNLQSVFRASKELKQRFQRLDCIYLNAGIMPNPQLNIKALFFGLFSRKVIHMFSTAEGLLTQ
GDKITADGLQEVFETNVFGHFILIRELEPLLCHSDNPSQLIWTSSRSARKSNFSLEDFQHSGK
KEPYSSSKYATDLLSVALNRNFNQQGLYSNVACPGTALTNLTYGILPPFIWTLLMPAILLLRF
FANAFTLTPYNGTEALVWLFHQKPESLNPLIKYLSATTGFGRNYIMTQKMDLDEDTAEKFYQK
LLELEKHIRVTIQKTDNQARLSGSCL

Important features:**Transmembrane domain:**

amino acids 234-254

N-glycosylation sites:

amino acids 37-41,178-182,229-233,263-267

Glycosaminoglycan attachment site:

amino acids 12-16

N-myristoylation sites:

amino acids 9-15,13-19,15-21,215-221,224-230

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FIGURE 257

CGGACGCGTG GGGGCCGT **ATG**CGCGGCTCTGTGGAGTGCACCTGGGGTTGGGGGCACTGTGCCC
CCAGCCCCCTGCTCCTTTGGACTCTACTTCTGTTTGCAGCCCCATTTGGCCTGCTGGGGGAGA
AGACCCGCCAGGTGTCTCTGGAGGTCATCCCTAACTGGCTGGGCCCCCTGCAGAACCTGCTTC
ATATACGGGCAGTGGGACCAATTCCACACTGCACTATGTGTGGAGCAGCCTGGGGCCTCTGG
CAGTGGTAATGGTGGCCACCAACACCCCCACAGCACCTGAGCATCAACTGGAGCCTCCTGC
TATCCCCTGAGCCCGATGGGGGCTGATGGTGTCTCCCTAAGGACAGCATTTCAGTTTTCTTCTG
CCCTTGTTTTTACCAGGCTGCTTGAGTTTGACAGCACCAACGTGTCCGATACGGCAGCAAAGC
CTTTGGGAAGACCATATCCTCCATACTCCTTGGCCGATTTCTCTTGGAACAACATCACTGATT
CATTGGATCCTGCCACCCTGAGTGCCACATTTCAAGGCCACCCCATGAACGACCCTACCAGGA
CTTTTGCCAATGGCAGCCTGGCCTTCAGGGTCCAGGCCTTTTCCAGGTCCAGCCGACCAGCCC
AACCCCTCGCCTCCTGCACACAGCAGACACCTGTCAGCTAGAGGTGGCCCTGATTGGAGCCT
CTCCCCGGGGAAACCGTTCCCTGTTTGGGCTGGAGGTAGCCACATTGGGCCAGGGCCCTGACT
GCCCCTCAATGCAGGAGCAGCACTCCATCGACGATGAATATGCACCGGCCGTCTTCCAGTTGG
ACCAGCTACTGTGGGGCTCCCTCCCATCAGGCTTTGCACAGTGGCGACCAGTGGCTTACTCCC
AGAAGCCGGGGGGCCGAGAATCAGCCCTGCCCTGCCAAGCTTCCCCTCTTCATCCTGCCTTAG
CATACTCTCTTCCCCAGTCACCCATTGTCCGAGCCTTCTTTGGGTCCCAGAATAACTTCTGTG
CCTTCAATCTGACGTTTCGGGGCTTCCACAGGCCCTGGCTATTGGGACCAACACTACCTCAGCT
GGTCGATGCTCCTGGGTGTGGGCTTCCCTCCAGTGGACGGCTTGTCCCCACTAGTCCTGGGCA
TCATGGCAGTGGCCCTGGGTGCCCCAGGGCTCATGCTGCTAGGGGGCGGCTTGGTTCTGCTGC
TGCACCACAAGAAGTACTCAGAGTACCAGTCCATAAAT **TAA**GGCCCGCTCTCTGGAGGGAAGG
ACATTACTGAACCTGTCTTGCTGTGCCTCGAAACTCTGGAGGTTGGAGCATCAAGTTCCAGCC
GGCCCCTTCACTCCCCCATCTTGCTTTTCTGTGGAACCTCAGAGGCCAGCCTCGACTTCCTGG
AGACCCCCAGGTGGGGCTTCCTTCATACTTTGTTGGGGGACTTTGGAGGCGGGCAGGGGACAG
GGCTATTGATAAGGTCCCCTTGGTGTTCCTTCTTGCATCTCCACACATTTCCCTTGGATGGG
ACTTGCAGGCCTAAATGAGAGGCATTCTGACTGGTTGGCTGCCCTGGAAGGCAAGAAAATAGA
TTTATTTTTTTTTCACAGGGGAAAAAAAAAAAAA

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FIGURE 258

MRGSVECTWGWGHCAPSPLLLWTLTLLFAAPFGLLGKTRQVSLEVIPNWLGPLQNLLHIRAVG
TNSTLHYVWSSLGPLAVVMVATNTPHSTLSINWSLLLSPEPDGGLMVLPKDSIQFSSALVFTR
LLEFDSTNVSDTAAKPLGRPYPPYSLADFSWNNITDSLDPATLSATFQGHMNDPTRTFANGS
LAFRVQAFSRSSRPAQPRLHTADTCQLEVALIGASPRGNRSLFGLEVATLGQGPDCPSMQE
QHSIDDEYAPAVFQLDQLLWGSLPSGFAQWRPVAYSQKPGGRESALPCQASPLHPALAYSLPQ
SPIVRAFFGSQNNFCAFNLTFGASTGPGYWDQHYLSWSMLLGVGFPVVDGLSPLVLGIMAVAL
GAPGLMLLGGLVLLLLHHKKYSEYQSIN

Important features:**Signal peptide:**

amino acids 1-35

Transmembrane domain:

amino acids 365-386

N-glycosylation sites:

amino acids 65-69, 95-99, 134-138, 159-163, 187-191, 230-234, 333-337

cAMP- and cGMP-dependent protein kinase phosphorylation site:

amino acids 397-401

N-myristoylation sites:

amino acids 3-9, 63-69, 235-241, 273-279, 292-298, 324-330

Leucine zipper pattern:

amino acids 371-393

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FIGURE 259

CAGGCGGGCCCCGCGCGGCAGGGCCCTGGACCCGCGCGGCTCCCGGGG**ATG**GTGAGCAAGGCGCTGCTGCGCCT
CGTGTCTGCCGTCAACCGCAGGAGGATGAAGCTGCTGCTGGGCATCGCCTTGCTGGCCTACGTCGCCTCTGTTTG
GGGCAACTTCGTTAATATGAGGTCTATCCAGGAAAATGGTGAACATAAAAATTGAAAGCAAGATTGAAGAGATGGT
TGAACCACTAAGAGAGAAAATCAGAGATTTAGAAAAAGCTTTACCCAGAAATACCCACCAGTAAAGTTTTTATC
AGAAAAGGATCGGAAAAGAATTTTGATAACAGGAGGCGCAGGGTTTCGTGGGCTCCCATCTAACTGACAACTCAT
GATGGACGGCCACGAGGTGACCGTGGTGGACAATTTCTTCACGGGCAGGAAGAGAAACGTGGAGCACTGGATCGG
ACATGAGAACTTCGAGTTGATTAACCACGACGTGGTGGAGCCCCCTCTACATCGAGGTTGACCAGATATACCATCT
GGCATCTCCAGCCTCCCCTCCAACTACATGTATAATCCTATCAAGACATTAAGACCAATACGATTGGGACATT
AAACATGTTGGGGCTGGCAAAACGAGTCGGTGCCCGTCTGCTCCTGGCCTCCACATCGGAGGTGTATGGAGATCC
TGAAGTCCACCCTCAAAGTGAGGATTACTGGGGCCACGTGAATCCAATAGGACCTCGGGCCTGCTACGATGAAGG
CAAACGTGTTGCAGAGACCATGTGCTATGCCTACATGAAGCAGGAAGGCGTGGAAGTGCGAGTGGCCAGAATCTT
CAACACCTTTGGGCCACGCATGCACATGAACGATGGGCGAGTAGTCAGCAACTTCATCCTGCAGGCGCTCCAGGG
GGAGCCACTCACGGTATACGGATCCGGGTCTCAGACAAGGGCGTTCCAGTACGTACGCGATCTAGTGAATGGCCT
CGTGGCTCTCATGAACAGCAACGTGAGCAGCCCGGTCAACCTGGGGAACCCAGAAGAACACACAATCCTAGAATT
TGCTCAGTTAATTAAAAACCTTGTTGGTAGCGGAAGTGAAATTCAGTTTCTCTCCGAAGCCCAGGATGACCCACA
GAAAAGAAAACCAGACATCAAAAAAGCAAAGCTGATGCTGGGGTGGGAGCCCGTGGTCCCGCTGGAGGAAGGTTT
AAACAAAGCAATTCCTACTTCCGTAAAGAACTCGAGTACCAGGCAAATAATCAGTACATCCCCAAACCAAAGCC
TGCCAGAATAAAGAAAGGACGGACTCGCCACAGC**TGA**ACTCCTCACTTTTAGGACACAAGACTACCATTTGTACAC
TTGATGGGATGTATTTTTGGCTTTTTTTTTGTTGTGCTTTAAAGAAAGACTTTAACAGGTGTGATGAAGAACAAC
TGGAATTTCACTCTGAAGCTTGCTTTAATGAAATGGATGTGCCTAAAAGCTCCCCTCAAAAACTGCAGATTTTG
CCTTGCACTTTTTGAATCTCTCTTTTTATGTAAATAGCGTAGATGCATCTCTGCGTATTTTCAAGTTTTTTTAT
CTTGCTGTGAGAGCATATGTTGTGACTGTGCTTGACAGTTTATTTACTGGTTTCTTTGTGAAGCTGAAAAGGAA
CATTAAAGCGGGACAAAAAATGCCGATTTTATTTATAAAAGTGGGTACTTAATAAATGAGTCGTTATACTATGCAT
AAAGAAAAATCCTAGCAGTATTGTCAGGTGGTGGTGCGCCGGCATTGATTTTAGGGCAGATAAAAGAATTCTGTG
TGAGAGCTTTATGTTTCTCTTTTAATTCAGAGTTTTTCCAAGGTCTACTTTTGAGTTGCAAACTTGACTTTGAAA
TATTCCTGTTGGTCATGATCAAGGATATTTGAAATCACTACTGTGTTTTGCTGCGTATCTGGGGCGGGGGCAGGT
TGGGGGGCACAAAGTTAACATATTCTTGGTTAACCATGGTTAAATATGCTATTTTAATAAAATATTGAAACTCA

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FIGURE 260

MVSKALLRLVSAVNRRRMKLLLGIALLAYVASVWGNFVNMRSIQENGELKIESKIEEMVEPLR
EKIRDLEKSFTQKYPPVKFLSEKDRKRILITGGAGFVGSHLTDKLMDGHEVTVVDNFFTGRK
RNVEHWIGHENFELINH DVVEPLYIEVDQIYHLASPPNYMYPNPIKTLKTNTIGTLNMLGL
AKRVGARLLLASTSEVYGDPEVHPQSEDYWGHVNPIGPRACYDEGKRVAETMCYAYMKQEGVE
VRVARIFNTFGPRMHMNDGRVVS NFILQALQGEPLTVYSGSQTRAFQYVSDLVNGLV ALMNS
NVSSPVNLGNPEEHTILEFAQLIKNLVSGSGSEIQFLSEAQDDPQKRKPDIKKAKLMLGWEPVV
PLEEGLNKAIHYFRKELEYQANNQYIPKPKPARIKKGRTRHS

Important features:**Signal peptide:**

amino acids 1-32

N-glycosylation site:

amino acids 316-320

Tyrosine kinase phosphorylation site:

amino acids 235-244

N-myristoylation sites:

amino acids 35-41, 101-107, 383-389

Amidation sites:

amino acids 123-127, 233-237

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FIGURE 261

GCGTGGTGCGGGGGCGTGGGGAAATCGGGTTGCCCCAGCCGTTACTGGTCCGCGCAGTCAGGG
CATCCTCCGCATCCTCCACATCCTTCC**ATG**GCTCTGAAGAATAAATTCAGTTGTTTATGGATC
TTGGGTCTGTGTTTGGTAGCCACTACATCTTCCAAAATCCCATCCATCACTGACCCACACTTT
ATAGACAACTGCATAGAAGCCCACAACGAATGGCGTGGCAAAGTCAACCCTCCCGCGGGCCGAC
ATGAAATACATGATTTGGGATAAAGGTTTAGCAAAGATGGCTAAAGCATGGGCAAACCAGTGC
AAATTTGAACATAATGACTGTTTGGATAAATCATATAAATGCTATGCAGCTTTTGAATATGTT
GGAGAAAATATCTGGTTAGGTGGAATAAAGTCATTCACACCAAGACATGCCATTACGGCTTGG
TATAATGAAACCCAATTTTATGATTTTGTAGTCTATCATGCTCCAGAGTCTGTGGCCATTAT
ACACAGTTAGTTTGGGCCAATTCATTTTATGTCGGTTGTGCAGTTGCAATGTGTCCTAACCTT
GGGGGAGCTTCAACTGCAATATTTGTATGCAACTACGGACCTGCAGGAAATTTTGCAAATATG
CCTCCTTACGCAAGAGGAGAATCTTGCTCTCTCTGCTCAAAAGAAGAGAAATGTGTAAAGAAC
CTCTGCAGGACTCCACAACCTTATTATACCTAACCAAAATCCATTTCTGAAGCCAACGGGGAGA
GCACCTCAGCAGACAGCCTTTAATCCATTCAGCTTAGGTTTTCTTCTTCTGAGAATCTTT**TAA**
TGTCATTTATATACAAAAGAAATTCTCAAATGTTAAAATAAAGGAATAGTTTATTGCTTAATA

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FIGURE 262

MALKNKFSCLWILGLCLVATTSSKIPSITDPHFIDNCIEAHNEWRGKVNPPAADMKYMIWDKG
LAKMAKAWANQCKFEHNDCLDKSYKCYAAFEYVGENIWLGGIKSFTPRHAITAWYNETQFYDF
DSLSCSRVCGHYTQLVWANSFYVGCAVAMCPNLGGASTAIFVCNYGPAGNFANMPPYARGESC
SLCSKEEKCCKVKNLCRTPQLIIPNQNPFLKPTGRAPQQTAFNPFSLGFLLLRIF

Important features:**Signal peptide:**

amino acids 1-23

N-glycosylation site:

amino acids 119-123

N-myristoylation sites:

amino acids 103-109,150-156,160-166,161-167,175-181

Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7 signature 1:

amino acids 136-156

Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7 signature 2:

amino acids 166-178

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FIGURE 263

CGCCCTCCGACCCGCCCCGCGGCGCATTGTGGGATCTGTCGGCTTGTCAGGTGGTGGAGGAAA
AGGCGCTCCGTC**ATG**GGGATCCAGACGAGCCCCGTCTGCTGGCCTCCCTGGGGGTGGGGCTG
GTCACTCTGCTCGGCCTGGCTGTGGGCTCCTACTTGTTTCGGAGGTCCCGCCGGCCTCAGGTC
ACTCTCCTGGACCCCAATGAAAAGTACCTGCTACGACTGCTAGACAAGACGACTGTGAGCCAC
AACACCAAGAGGTTCCGCTTTGCCCTGCCACCGCCCCACCACACTCTGGGGCTGCCTGTGGGC
AAACATATCTACCTCTCCACCCGAATTGATGGCAGCCTGGTCATCAGGCCATACACTCCTGTC
ACCAGTGATGAGGATCAAGGCTATGTGGATCTTGTCATCAAGGTCTACCTGAAGGGTGTGCAC
CCCAAATTTCTGAGGGAGGGAAGATGTCTCAGTACCTGGATAGCCTGAAGGTGGGGATGTG
GTGGAGTTTCGGGGGCCAAGCGGGTTGCTCACTTACACTGGAAAAGGGCATTTTAACATTTCAG
CCCAACAAGAAATCTCCACCAGAACCCCGAGTGGCGAAGAACTGGGAATGATTGCCGGCGGG
ACAGGAATCACCCCAATGCTACAGCTGATCCGGGCCATCCTGAAAGTCCCTGAAGATCCAACC
CAGTGCTTTCTGCTTTTTGCCAACCAGACAGAAAAGGATATCATCTTGCGGGAGGACTTAGAG
GAACTGCAGGCCCCGCTATCCCAATCGCTTTAAGCTCTGGTTCCTCTGGATCATCCCCCAAAA
GATTGGGCCTACAGCAAGGGCTTTGTGACTGCCGACATGATCCGGGAACACCTGCCCGCTCCA
GGGGATGATGTGCTGGTACTGCTTTGTGGGCCACCCCCAATGGTGCAGCTGGCCTGCCATCCC
AACTTGGACAAACTGGGCTACTCACAAAAGATGCGATTACCTAC**TGA**GCATCCTCCAGCTTC
CCTGGTGCTGTTTCGCTGCAGTTGTTCCCCATCAGTACTCAAGCACTATAAGCCTTAGATTCCCT
TTCCTCAGAGTTTCAGGTTTTTTTCAGTTACATCTAGAGCTGAAATCTGGATAGTACCTGCAGG
AACAAATATTCTGTAGCCATGGAAGAGGGCAAGGCTCAGTCACTCCTTGGATGGCCTCCTAAA
TCTCCCCGTGGCAACAGGTCCAGGAGAGGGCCCATGGAGCAGTCTCTTCCATGGAGTAAGAAGG
AAGGGAGCATGTACGCTTGGTCCAAGATTGGCTAGTTCCTTGATAGCATCTTACTCTCACCTT
CTTTGTGTCTGTGATGAAAGGAACAGTCTGTGCAATGGGTTTTACTTAAACTTCACTGTTCAA
CCTATGAGCAAATCTGTATGTGTGAGTATAAGTTGAGCATAGCATACTTCCAGAGGTGGTNTT
ATGGAGATGGCAAGAAAGGAGGAAATGATTTCTTCAGATNTCAAAGGAGTCTGAAATATCATA
TTTCTGTGTGTGTCTCTCTCAGCCCCTGCCAGGCTAGAGGGAAACAGCTACTGATAATCGAA
AACTGCTGTTTTGTGGCANGAACCCCTGGCTGTGCAAATAAATGGGGCTGAGGCCCTGTGTGA
TATTGAAGA

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FIGURE 264

MGIQTSPVLLASLGVGLVTLLGLAVGSYLVRRSRPQVTLLDPNEKYLLRLLDKTTVSHNTR
FRFALPTAHTLGLPVGKHIYLSTRIDGSLVIRPYTPVTSDEDQGYVDLVIKVYLKGVHPKFP
EGGKMSQYLDLKVGDVVEFRGPSGLLTYTGKGHFNIQPNKSPPEPRVAKKLGMIAGGTGIT
PMLQLIRAILKVPEDPTQCFLLFANQTEKDIIILREDLEELQARYPNRFKLWFTLDHPPKDWAY
SKGFVTADMIREHLPAPGDDVLVLLCGPPPMVQLACHPNLDKLGYSQKMRFTY

Important features:**Signal peptide:**

amino acids 1-26

N-glycosylation site:

amino acids 214-218

N-myristoylation sites:

amino acids 22-28, 76-82, 128-134, 180-186

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FIGURE 265

CCCGTGCCAAGAGTGACGTAAGTACCGCCTATAGAGTCTATAGGCCCACTTGGCTTCGTTAGA
ACGCGGCTACAATTAATACATAACCTTATGTATCATACACATACGATTTAGGTGACACTATAG
AATAACATCCACTTTGCCTTTCTCTCCACAGGTGTCCACTCCCAGGTCCAACTGCACCTCGGT
TCTATCGATAATCTCAGCACCAGCCACTCAGAGCAGGGCACG**ATG**TTGGGGGCCCCGCCTCAGG
CTCTGGGTCTGTGCCTTGTGCAGCGTCTGCAGCATGAGCGTCCTCAGAGCCTATCCCAATGCC
TCCCCACTGCTCGGCTCCAGCTGGGGTGGCCTGATCCACCTGTACACAGCCACAGCCAGGAAC
AGCTACCACCTGCAGATCCACAAGAATGGCCATGTGGATGGCGCACCCCATCAGACCATCTAC
AGTGCCCTGATGATCAGATCAGAGGATGCTGGCTTTGTGGTGATTACAGGTGTGATGAGCAGA
AGATACCTCTGCATGGATTTTCAGAGGCAACATTTTTTGGATCACACTATTTTCGACCCGGAGAAC
TGCAGGTTCCAACACCAGACGCTGGAAAACGGGTACGACGTCTACCACTCTCCTCAGTATCAC
TTCCTGGTCAGTCTGGGCCGGGCGAAGAGAGCCTTCCTGCCAGGCATGAACCCACCCCGTAC
TCCCAGTTCCTGTCCCGGAGGAACGAGATCCCCCTAATTCACCTCAACACCCCCATACCACGG
CGGCACACCCGGAGCGCCGAGGACGACTCGGAGCGGGACCCCCTGAACGTGCTGAAGCCCCGG
GCCCCGATGACCCCGGCCCGGCCCTCCTGTTTACAGGAGCTCCCGAGCGCCGAGGACAACAGC
CCGATGGCCAGTGACCCATTAGGGGTGGTCAGGGGCGGTTCGAGTGAACACGCACGCTGGGGGA
ACGGGCCCCGAAGGCTGCCGCCCTTCGCCAAGTTCATC**TAG**GGTCGCTGG

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FIGURE 266

MLGARLRLWVCALCSVCSMSVLRAYPNASPLLGSWSGGLIHLYTATARNSYHLQIHKNGHVDG
APHQTIYSALMIRSEDAGFVVITGVMSRRYLCMDFRGNIFGSHYFDPENCRFQHQTLNGYDV
YHSPQYHFLVSLGRAKRAFLPGMNPPPYSQLSRNEIPLIHFNTPIPRRHTRSAEDDSERDP
LNVLKPRARMT PAPASCSQELPSAEDNSPMASDPLGVVRGGRVNT HAGGTGPEGCRPF AKFI

Important features:**Signal peptide:**

amino acids 1-24

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 175-179

N-myristoylation site.

amino acids 33-39, 100-106, 225-231, 229-235

HBGF/FGF family proteins

amino acids 73-124

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FIGURE 267

GGCTGAGGGGAGGCCCGAGCCTTTCTGGGGCCTGGGGGATCCTCTTGCACTGGTGGGTGGAGAGAAGCGCCTGC
AGCCAACCAGGGTCAGGCTGTGCTCACAGTTTCTCTGGCGGCATGTAAAGGCTCCACAAAGGAGTTGGGAGTTC
AAATGAGGCTGCTGCGGACGGCCTGAGGATGGACCCCAAGCCCTGGACCTGCCGAGCGTGGCACTGAGGCAGCGG
CTGACGCTACTGTGAGGGAAAGAAGGTTGTGAGCAGCCCCGAGGACCCCTGGCCAGCCCTGGCCCCAGCCTCTG
CCGGAGCCCTCTGTGGAGGCAGAGCCAGTGGAGCCCAGTGAGGCAGGGCTGCTTGGCAGCCACCGGCCTGCAACT
CAGGAACCCCTCCAGAGGCCATGGACAGGCTGCCCCGCTGACGGCCAGGGTGAAGCATGTGAGGAGCCGCCCCGG
AGCCAAGCAGGAGGGAAGAGGCTTTCATAGATTCTATTACAAAGAATAACCACCATTTTGCAAGGACCATGAGG
CCACTGTGCGTGACATGCTGGTGGCTCGGACTGCTGGCTGCCATGGGAGCTGTTGCAGGCCAGGAGGACGGTTTT
GAGGGCACTGAGGAGGGCTCGCCAAGAGAGTTCAATTTACCTAAACAGGTACAAGCGGGCGGGCGAGTCCCAGGAC
AAGTGCACCTACACCTTCATTGTGCCCCAGCAGCGGGTCAACGGGTGCCATCTGCGTCAACTCCAAGGAGCCTGAG
GTGCTTCTGGAGAACCGAGTGCATAAGCAGGAGCTAGAGCTGCTCAACAATGAGCTGCTCAAGCAGAAGCGGCAG
ATCGAGACGCTGCAGCAGCTGGTGGAGGTGGACGGCGGCATTGTGAGCGAGGTGAAGCTGCTGCGCAAGGAGAGC
CGCAACATGAACTCGCGGGTCACGCAGCTCTACATGCAGCTCCTGCACGAGATCATCCGCAAGCGGGACAACGCG
TTGGAGCTCTCCCAGCTGGAGAACAGGATCCTGAACCAGACAGCCGACATGCTGCAGCTGGCCAGCAAGTACAAG
GACCTGGAGCACAAGTACCAGCACCTGGCCACACTGGCCCACAACCAATCAGAGATCATCGCGCAGCTTGAGGAG
CACTGCCAGAGGGTGCCCTCGGCCAGGCCCGTCCCCAGCCACCCCCCGCTGCCCCGCCCCGGGTCTACCAACCA
CCCACCTACAACCGCATCATCAACCAGATCTCTACCAACGAGATCCAGAGTGACCAGAACCTGAAGGTGCTGCCA
CCCCCTCTGCCCCTATGCCCCTCTCACCAGCCTCCCATCTTCCACCGACAAGCCGTGGGGCCCATGGAGAGAC
TGCCTGCAGGCCCTGGAGGATGGCCACGACACCAGCTCCATCTACCTGGTGAAGCCGGAGAACACCAACCGCCTC
ATGCAGGTGTGGTGCAGACCAGAGACACGACCCCGGGGGCTGGACCGTCATCCAGAGACGCCTGGATGGCTCTGTT
AACTTCTTCAGGAACTGGGAGACGTACAAGCAAGGGTTTGGGAACATTGACGGCGAATACTGGCTGGGCCTGGAG
AACATTTACTGGCTGACGAACCAAGGCAACTACAACTCCTGGTGACCATGGAGGACTGGTCCGGCCGCAAGTC
TTTGCAGAATACGCCAGTTTCCGCCTGGAACCTGAGAGCGAGTATTATAAGCTGCGGCTGGGGCGCTACCATGGC
AATGCGGGTGACTCCTTTACATGGCACAACGGCAAGCAGTTACCAACCCTGGACAGAGATCATGATGTCTACACA
GGAACTGTGCCCCTACCAGAAGGGAGGCTGGTGGTATAACGCCTGTGCCCCTCCAACCTCAACGGGGTCTGG
TACCGCGGGGGCCATTACCGGAGCCGCTACCAGGACGGAGTCTACTGGGCTGAGTTCCGAGGAGGCTCTTACTCA
CTCAAGAAAGTGGTGATGATGATCCGACCGAACCCCAACACCTTCCACTAAGCCAGCTCCCCCTCCTGACCTCTC
GTGGCCATTGCCAGGAGCCCACCCTGGTCACGCTGGCCACAGCACAAAGAACAACCTCCTCACCAGTTCATCCTGA
GGCTGGGAGGACCGGGATGCTGGATTCTGTTTTCCGAAGTCACTGCAGCGGATGATGGAAGTGAATCGATACGGT
GTTTTCTGTCCCTCCTACTTTCCTTCACACCAGACAGCCCCCTCATGTCTCCAGGACAGGACAGGACTACAGACAA
CTCTTTCTTTAAATAAAATTAAGTCTCTACAATAAAAAAAA

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FIGURE 268

MRPLCVTCWWLGLLAAMGAVAGQEDGFEGTEEGSPREFIYLNRYKRAGESQDKCTYTFIVPQQ
RVTGAICVNSKEPEVLLLENRVHKQELELLNNELLKQKRQIETLQQLEVDGGIVSEVKLLRKE
SRNMNSRVTQLYMQLLHEIIRKRDNALELSQLENRIINQITADMLQLASKYKDLEHKYQHLATL
AHNQSEIIAQLEEHQCQRVPSARVPVQPPPAAPPRVYQPPTYNRIINQISTNEIQSDQNLKVL
PPLPTMPTLTSLPSSTDKPSGPWRDCLQALEDGHDTSSIYLVKPENTNRLMQVWCDQRHDPGG
WTVIQRRLDGSVNFFRNWETKYQGFGNIDGEYWLGLENIYWLTNQGNKYKLLVTMEDWSGRKVF
AEYASFRLEPESEYYKLRLGRYHGNAGDSFTWHNGKQFTTLDRDHDVYTGNCAGHYQKGGWWYN
ACAHSNNGVWYRGGHYRSRYQDGVYWAEFRGGSYSLKKVMMIRPNPNTFH

Important features:**Signal peptide:**

amino acids 1-22

N-glycosylation sites:

amino acids 164-168, 192-196

cAMP- and cGMP-dependent protein kinase phosphorylation site:

amino acids 124-128

Tyrosine kinase phosphorylation sites:

amino acids 177-184, 385-393, 385-394, 461-468

N-myristoylation sites:amino acids 12-18, 18-24, 22-28, 29-35, 114-120, 341-347, 465-471,
473-479**Amidation site:**

amino acids 373-377

Fibrinogen beta and gamma chains C-terminal domain signature:

amino acids 438-451

Fibrinogen beta and gamma chains C-terminal domain proteins:

amino acids 305-343, 365-402, 411-424, 428-458

Trehalase proteins:

amino acids 275-292

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FIGURE 269

GCCGAGCTGAGCGGATCCTCACATGACTGTGATCCGATTCTTTCCAGCGGCTTCTGCAACCAA
GCGGGTCTTACCCCCGGTCCTCCGCGTCTCCAGTCCTCGCACCTGGAACCCCAACGTCCCCGA
GAGTCCCCGAATCCCCGCTCCCAGGCTACCTAAGAGGATGAGCGGTGCTCCGACGGCCGGGGC
AGCCCTGATGCTCTGCGCCGCCACCGCCGTGCTACTGAGCGCTCAGGGCGGACCCGTGCAGTC
CAAGTCGCCGCGCTTTGCGTCCTGGGACGAGATGAATGTCCTGGCGCACGGACTCCTGCAGCT
CGGCCAGGGGCTGCGCGAACACGCGGAGCGCACCCGCAGTCAGCTGAGCGCGCTGGAGCGGCG
CCTGAGCGCGTGCGGGTCCGCCTGTCAGGGAACCGAGGGGTCCACCGACCTCCCGTTAGCCCC
TGAGAGCCGGGTGGACCCTGAGGTCCTTCACAGCCTGCAGACACAACCTCAAGGCTCAGAACAG
CAGGATCCAGCAACTCTTCCACAAGGTGGCCCAGCAGCAGCGGCACCTGGAGAAGCAGCACCT
GCGAATTCAGCATCTGCAAAGCCAGTTTGGCCTCCTGGACCACAAGCACCTAGACCATGAGGT
GGCCAAGCCTGCCCCGAAGAAAGAGGCTGCCCCGAGATGGCCCAGCCAGTTGACCCGGCTCACAA
TGTCAGCCGCTGACCCGGCTGCCAGGGATTGCCAGGAGCTGTTCCAGGTTGGGGAGAGGCA
GAGTGGACTATTTGAAATCCAGCCTCAGGGGTCTCCGCCATTTTTGGTGAACCTGCAAGATGAC
CTCAGATGGAGGCTGGACAGTAATTCAGAGGCGCCACGATGGCTCAGTGGACTTCAACCGGCC
CTGGGAAGCCTACAAGGCGGGGTTTGGGGATCCCCACGGCGAGTTCTGGCTGGGTCTGGAGAA
GGTGCATAGCATCACGGGGGACCGCAACAGCCGCCTGGCCGTGCAGCTGCGGGACTGGGATGG
CAACGCCGAGTTGCTGCAGTTCTCCGTGCACCTGGGTGGCGAGGACACGGCCTATAGCCTGCA
GCTCACTGCACCCGTGGCCGGCCAGCTGGGCGCCACCACCGTCCCACCCAGCGGCCTCTCCGT
ACCCTTCTCCACTTGGGACCAGGATCACGACCTCCGCAGGGACAAGAAGTGCGCCAAGAGCCT
CTCTGGAGGCTGGTGGTTTGGCACCTGCAGCCATTCCAACCTCAACGGCCAGTACTTCCGCTC
CATCCCACAGCAGCGGCAGAAGCTTAAGAAGGGAATCTTCTGGAAGACCTGGCGGGGCCGCTA
CTACCCGCTGCAGGCCACCACCATGTTGATCCAGCCCATGGCAGCAGAGGCAGCCTCCTAGCG
TCCTGGCTGGGCCTGGTCCCAGGCCCACGAAAGACGGTGACTCTTGGCTCTGCCCAGGATGT
GGCCGTTCCTGCCTGGGCAGGGGCTCCAAGGAGGGGCCATCTGGAACTTGTGGACAGAGAA
GAAGACCACGACTGGAGAAGCCCCCTTTCTGAGTGCAGGGGGGCTGCATGCGTTGCCTCCTGA
GATCGAGGCTGCAGGATATGCTCAGACTCTAGAGGCGTGGACCAAGGGGCATGGAGCTTCACT
CCTTGCTGGCCAGGGAGTTGGGGACTCAGAGGGACCACTTGGGGCCAGCCAGACTGGCCTCAA
TGGCGGACTCAGTCACATTGACTGACGGGGACAGGGCTTGTGTGGGTGAGAGCGCCCTCAT
GGTGCTGGTGCTGTTGTGTGTAGGTCCCCTGGGGACACAAGCAGGCGCCAATGGTATCTGGGC
GGAGCTCACAGAGTTCTTGGAATAAAAGCAACCTCAGAACAC

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FIGURE 270

MTVIRFFPAASATKRVLPPVLRVSSPRTWNPVPESPRIPAPRLPKRMSGAPTAGAALMLCAA
TAVLLSAQGGPVQSKSPRFASWDEMNVLAHGLLQLGQGLREHAERTRSQLSALERRLSACGSA
CQGTEGSTDLPLAPESRVDPEVLHSLQTQLKAQNSRIQQLFHKVAQQQRHLEKQHLRIQHLQS
QFGLLDHKHLDHEVAKPARRKRLPEMAQPVDPAHNVSRHLRLPRDCQELFQVGERQSGLFQEIQ
PQGSPPFLVNCKMTSDGGWTVIQRRHDGSVDFNRPWEAYKAGFGDPHGEFWLGLEKVHSITGD
RNSRLAVQLRDWDGNAELLQFSVHLGGEDTAYSLQLTAPVAGQLGATTVPVPSGLSVPFSTWDQ
DHDLRDKNCAKSLSGGWFGTCSHSNLNGQYFRSIPQQRQKLKKGIFWKTWRGRYYPLQATT
MLIQPMAAEAAS

Important features:**Signal peptide:**

Amino acids 1-13

Transmembrane domain:

Amino acids 53-70

N-glycosylation site:

Amino acids 224-228

cAMP- and cGMP-dependent protein kinase phosphorylation sites:

Amino acids 46-50;118-122

N-myristoylation sites:

Amino acids 50-56;129-135;341-347;357-363

Fibrinogen beta and gamma chains C-terminal domain signature:

Amino acids 396-409

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FIGURE 271

CGGACGCGTG GGGGAAACCCTTCCGAGAAAACAGCAACAAGCTGAGCTGCTGTGACAGAGGGG
AACAAGATGGCGGCGCCGAAGGGGAGCCTCTGGGTGAGGACCCAACTGGGGCTCCCGCCGCTG
CTGCTGCTGACCATGGCCTTGGCCGGAGGTTTCGGGGACCGCTTCGGCTGAAGCATTTGACTCG
GTCTTGGGTGATACGGCGTCTTGCCACCGGGCCTGTCAGTTGACCTACCCCTTGACACACCTAC
CCTAAGGAAGAGGAGTTGTACGCATGTCAGAGAGGTTGCAGGCTGTTTTCAATTTGTCAGTTT
GTGGATGATGGAATTGACTTAAATCGAACTAAATTGGAATGTGAATCTGCATGTACAGAAGCA
TATCCCAATCTGATGAGCAATATGCTTGCCATCTTGGTTGCCAGAATCAGCTGCCATTCGCT
GAACTGAGACAAGAACAACCTTATGTCCCTGATGCCAAAAATGCACCTACTCTTTCCTCTAACT
CTGGTGAGGTCATTCTGGAGTGACATGATGGACTCCGCACAGAGCTTCATAACCTCTTCATGG
ACTTTTTATCTTCAAGCCGATGACGGAAAAATAGTTATATTCCAGTCTAAGCCAGAAATCCAG
TACGCACCACATTTGGAGCAGGAGCCTACAAATTTGAGAGAATCATCTCTAAGCAAAATGTCC
TATCTGCAAATGAGAAATTCACAAGCGCACAGGAATTTTCTTGAAGATGGAGAAAGTGATGGC
TTTTTAAGATGCCTCTCTCTTAACTCTGGGTGGATTTTAACTACAACCTCTTGTCTCTCGGTG
ATGGTATTGCTTTGGATTTGTTGTGCAACTGTTGCTACAGCTGTGGAGCAGTATGTTCCCTCT
GAGAAGCTGAGTATCTATGGTGACTTGGAGTTTATGAATGAACAAAAGCTAAACAGATATCCA
GCTTCTTCTCTTGTGGTTGTTAGATCTAAACTGAAGATCATGAAGAAGCAGGGCCTCTACCT
ACAAAAGTGAATCTTGCTCATTCTGAAATTTAAGCATTTTTCTTTTAAAGACAAGTGTAATA
GACATCTAAATTCCTCCTCATAGAGCTTTTAAATGGTTTCATTGGATATAGGCCTTAAG
AAATCACTATAAAATGCAAATAAAGTTACTCAAATCTGTG

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FIGURE 272

MAAPKGS LWVRTQLGLPPLLLLTMALAGGSGTASAEAFDSVLGDTASCHRA CQLTYPLHTYPK
EEELYACQRGCR LFSICQFVDDGIDLNR TKLECESACTEAYSQSDEQYACHLGCQNQLPFAEL
RQEQLMSLMPKMHL LFPLTLVRSFWSDMMDSAQS FITSSWTFYLQADDGKIVIFQSKPEIQYA
PHLEQEPTNLRESSLSKMSYLQMRNSQAHRNFLEDGESDGFLRCLSLNSGWILTTTLVLSVMV
LLWICCATVATAVEQYVPSEKLSIYGDLEFMNEQKLNRYPASSLVVVR SKTEDHEEAGPLPTK
VNLAHSEI

Important features:**Signal peptide:**

amino acids 1-31

Transmembrane domain:

amino acids 241-260

N-glycosylation site:

amino acids 90-94

N-myristoylation sites:

amino acids 28-34, 29-35, 31-37, 86-92

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FIGURE 273

CCCACGCGTCCGAACCTCTCCAGCGATGGGAGCCGCCCGCCTGCTGCCCCAACCTCACTCTGTG
CTTACAGCTGCTGATTCTCTGCTGTCAAACCTCAGTACGTGAGGGACCAGGGCGCCATGACCGA
CCAGCTGAGCAGGCGGCAGATCCGCGAGTACCAACTCTACAGCAGGACCAGTGGCAAGCACGT
GCAGGTCACCGGGCGTCGCATCTCCGCCACCGCCGAGGACGGCAACAAGTTTGCCAAGCTCAT
AGTGGAGACGGACACGTTTGGCAGCCGGGTTCGCATCAAAGGGGCTGAGAGTGAGAAGTACAT
CTGTATGAACAAGAGGGGCAAGCTCATCGGGAAGCCCAGCGGGAAGAGCAAAGACTGCGTGTT
CACGGAGATCGTGCTGGAGAACAACCTATACGGCCTTCCAGAACGCCCCGGCACGAGGGCTGGTT
CATGGCCTTCACGCGGCAGGGGCGGCCCGCCAGGCTTCCCGCAGCCGCCAGAACCAGCGCGA
GGCCCCACTTCATCAAGCGCCTCTACCAAGGCCAGCTGCCCTTCCCCAACCCACGCCGAGAAGCA
GAAGCAGTTCGAGTTTGTGGGCTCCGCCCCCACCCGCCGGACCAAGCGCACACGGCGGGCCCCA
GCCCCCTCACGTAGTCTGGGAGGCAGGGGGCAGCAGCCCCTGGGCGCCTCCCCACCCCTTTCC
CTTCTTAATCCAAGGACTGGGCTGGGGTGGCGGGAGGGGAGCCAGATCCCCGAGGGAGGACCC
TGAGGGCCGCGAAGCATCCGAGCCCCCAGCTGGGAAGGGGCAGGCCGGTGCCCCAGGGGCGGC
TGGCACAGTGCCCCCTTCCCGGACGGGTGGCAGGCCCTGGAGAGGAACTGAGTGTACCCCTGA
TCTCAGGCCACCAGCCTCTGCCGGCCTCCAGCCGGGCTCCTGAAGCCCGCTGAAAGGTCAGC
GACTGAAGGCCTTGCAGACAACCGTCTGGAGGTGGCTGTCCTCAAAATCTGCTTCTCGGATCT
CCCTCAGTCTGCCCCCAGCCCCCAAACCTCCTCCTGGCTAGACTGTAGGAAGGGACTTTTGTTT
GTTTGTTTGTTTCAGGAAAAAAGAAAGGGAGAGAGAGGAAATAGAGGGTTGTCCACTCCTCA
CATTCCACGACCCAGGCCTGCACCCCAACCCCAACTCCCAGCCCCGAATAAAACCATTTTCC
TGC

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FIGURE 274

MGAARLLPNLTLCQLLLILCCQTQYVRDQGAMTDQLSRRQIREYQLYSRTSGKHVQVTGRRIS
ATAEDGNKFAKLIVETDTFGSRVRIKGAESEKYICMNKRGLIGKPSGKSKDCVFTEIVLENN
YTAFQONARHEGWFMFAFTRQGRPRQASRSRQNQREAHFIKRLYQGQLPFPNHA EKQKQFEFVGS
APTRRTKRTRRPQPLT

Important features:**Signal peptide:**

Amino acids 1-22

N-glycosylation site.

amino acids 9-13, 126-130

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 60-64

Casein kinase II phosphorylation site.

amino acids 65-69

Tyrosine kinase phosphorylation site.

amino acids 39-48, 89-97

N-myristoylation site.

amino acids 69-75, 188-194

Amidation site.

amino acids 58-62

HBGF/FGF family signature.

amino acids 103-128

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FIGURE 275

TATTTACCATATCAGATTCACATTCAGTCCTCAGCAAAATGAAGGGCTCCATTTTCACTCTGT
TTTTATTCTCTGTCCTATTTGCCATCTCAGAAAGTGC GGAGCAAGGAGTCTGTGAGACTCTGTG
GGCTAGAATACATACGGACAGTCATCTATATCTGTGCTAGCTCCAGGTGGAGAAGGCATCTGG
AGGGGATCCCTCAAGCTCAGCAAGCTGAGACAGGAAACTCCTTCCAGCTCCACATAAACGTG
AGTTTTCTGAGGAAAATCCAGCGCAAAACCTTCCGAAGGTGGATGCCTCAGGGGAAGACCGTC
TTTGGGGTGGACAGATGCCCCACTGAAGAGCTTTGGAAGTCAAAGAAGCATTCACTGATGTCAA
GACAAGATTTACAAACTTTGTGTTGCACTGATGGCTGTTCCATGACTGATTTGAGTGCTCTTT
GCTAAGACAAGAGCAAATACCCAATGGGTGGCAGAGCTTTATCACATGTTTAATTACAGTGTT
TTACTGCCTGGTAGAACACTAATATTGTGTTATTAAAATGATGGCTTTTGGGTAGGC AAAACT
TCTTTTCTAAAAGGTATAGCTGAGCGGTTGAAACCACAGTGATCTCTATTTTCTCCCTTTGCC
AAGGTTAATGAACTGTTCTTTTCAAATTCTACTAATGCTTTGAAATTTCAAATGCTGCGCAAA
ATTGCAATAAAAATGCTATAAA

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FIGURE 276

MKGSIFTLFLFSVLFAISEVRSKESVRLCGLEYIRTVIYICASSRWRRHLEGIPQAQQAETGN
SFQLPHKREFSEENPAQNLPKVDASGEDRLWGGQMPTEELWKS KHSVMSRQDLQTLCTDGC
SMTDLSALC

Important features:**Signal sequence:**

amino acids 1-18

cAMP- and cGMP-dependent protein kinase phosphorylation site:

amino acids 107-111

N-myristoylation sites:

amino acids 3-9,52-58,96-102,125-131

Insulin family signature:

amino acids 121-136

Insulin family proteins:

amino acids 28-46

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FIGURE 277

GCAGCTGGTTACTGCATTTCTCCATGTGGCAGACAGAGCAAAGCCACAACGCTTTCTCTGCTGGATTAAAGACGG
CCCACAGACCAGAACTTCCACTATACTACTTAAAATTACATAGGTGGCTTGTCAAATTCAATTGATTAGTATTGT
AAAAGGAAAAAGAAAGTTCCCTTCTTACAGCTTGGATTCAACGGTCCAAAACAAAAATGCAGCTGCCATTAAAGTCT
CAGATGAACAACTTCTACACTGATTTTTTAAAATCAAGAATAAGGGCAGCAAGTTTCTGGATTCACTGAATCAAC
AGACACAAAAAGCTGGCAATATAGCAACTATGAAGAGAAAAGCTACTAATAAAAATTAACCCAACGCATAGAAGAC
TTTTTTTTTCTCTTCTAAAAACAACCTAAGTAAAGACTTAAATTTAAACACATCATTTTACAACCTCATTTTCAAAAT
GAAGACTTTTACCTGGACCCTAGGTGTGCTATTCTTCTACTAGTGGACACTGGACATTGCAGAGGTGGACAATT
CAAAATTAATAAAAAATAAACAGAGAAGATACCCTCGTGCCACAGATGGTAAAGAGGAAGCAAAGAAATGTGCATA
CACATTCTGGTACCTGAACAAAGAATAACAGGGCCAATCTGTGTCAACACCAAGGGGCAAGATGCAAGTACCAT
TAAAGACATGATCACCAGGATGGACCTTGAAAACCTGAAGGATGTGCTCTCCAGGCAGAAGCGGGAGATAGATGT
TCTGCAACTGGTGGTGGATGTAGATGGAACATTGTGAATGAGGTAAAGCTGCTGAGAAAGGAAAGCCGTAACAT
GAACTCTCGTGTTACTCAACTCTATATGCAATTATTACATGAGATTATCCGTAAGAGGGGATAATTCACTTGAAC
TTCCCAACTGGAAAACAAAATCCTCAATGTCACCACAGAAATGTTGAAGATGGCAACAAGATACAGGGAACTAGA
GGTGAAATACGCTTCCTTGACTGATCTTGTCAATAACCAATCTGTGATGATCACTTTGTTGGAAGAACAGTGCTT
GAGGATATTTTCCCGACAAGACACCCATGTGTCTCCCCCACTTGTCCAGGTGGTGGCCACAACATATTTCTAACAG
CCAACAGTATACTCCTGGTCTGCTGGGAGGTAACGAGATTGAGAGGGATCCAGGTTATCCCAGAGATTTAATGCC
ACCACCTGATCTGGCAACTTCTCCACCAAAAGCCCTTTCAAGATACCACCGGTAACTTTCATCAATGAAGGACC
ATTCAAAGACTGTCAGCAAGCAAAGAAGCTGGGCATTCCGGTCAGTGGGATTTATATGATTAAACCTGAAAAACAG
CAATGGACCAATGCAGTTATGGTGTGAAAACAGTTTGGACCTGGGGGTGGACTGTTATTGAGAAAAGAACAGA
CGGCTCTGTCAACTTCTTCAGAAATTGGGAAAATTATAAGAAAGGGTTTGGAAACATTGACGGAGAATACTGGCT
TGGACTGGAAAATATCTATATGCTTAGCAATCAAGATAATTACAAGTTATTGATTGAATTAGAAGACTGGAGTGA
TAAAAAGTCTATGCAGAATACAGCAGCTTTCGTCTGGAACCTGAAAGTGAATTCTATAGACTGCGCCTGGGAAC
TTACCAGGGAAATGCAGGGGATTCTATGATGTGGCATAATGGTAAACAATTCACCACACTGGACAGAGATAAAGA
TATGTATGCAGGAACTGCGCCCACTTTTATAAAGGAGGCTGGTGGTACAATGCCTGTGCACATTCTAACCTAAA
TGGAGTATGGTACAGAGGAGGCCATTACAGAAGCAAGCACCAAGATGGAATTTTCTGGGCCGAATACAGAGGCGG
GTCATACTCCTTAAGAGCAGTTCAGATGATGATCAAGCCTATTGACTGAAGAGAGACACTGCCAATTTAAATGA
CACAGAACTTTGTACTTTTCAGCTCTTAAAAATGTAATGTTACAGTATGATATTACTTGGCACAATTTATTTCTAC
ACAGAAAGTTTTTTAAAATGAATTTTACCCTAAGTATAAAGGGAAACCTATAAATGTAGTTTCATCTGTCTCAAT
TACTGCAGAAAATTATGTGTATCCACAACCTAGTTATTTTAAAAATTTATGTTGACTAAATACAAAGTTTGTTC
TAAAATGTAAATATTTGCCACAATGTAAAGCAAATCTTAGCTATATTTTAAATCATAAATAACATGTTCAAGATA
CTTAACAATTTATTTAAAATCTAAGATTGCTCTAACGTCTAGTGAAAAAAATATTTTTTAAATTTTCAAGCAATA
ATGCATTTTATTTTATAAAAAATACAGACAGAAAATTAGGGAGAACTTCTAGTTTGGCAATAGAAAATGTTCTT
CCATTGAATAAAAAGTTATTTCAAATTGAATTTGTGCCTTTTACACGTAATGATTAAATCTGAATTCCTAATAATA
TATCCTATGCTGATTTTCCCAAAACATGACCCATAGTATTAATAACATATCATTTTTTAAAAATAAAAAAAACCC
AAAAATAATGCATGCATAATTTAAATGGTCAATTTATAAAGACAAATCTATGAATGAATTTTTTCAGTGTTATCTT
CATATGATATGCTGAACACCAAAATCTCCAGAAATGCATTTTATGTAGTTCTAAAATCAGCAAAATATTGGTATT
ACAAAAATGCAGAATATTTAGTGTGCTACAGATCTGAATTATAGTTCTAATTTATTATTACTTTTTTTCTAATTT
ACTGATCTTACTACTACAAAGAAAAAAAACCCAACCCATCTGCAATTCAAATCAGAAAGTTTGGACAGCTTTAC
AAGTATTAGTGCATGCTCAGAACAGGTGGGACTAAAACAAACTCAAGGAAGTGTGGCTGTTTTCCCGATACTGA
GAATTC AACAGCTCCAGAGCAGAAGCCACAGGGGCATAGCTTAGTCCAACTGCTAATTTTCAATTTTACAGTGTAT
GTAACGCTTAGTCTCACAGTGTCTTTAACTCATCTTTGCAATCAACAACTTTACTAGTGACTTTCTGGAACAATT
TCCTTTTCAAGGAATACATATTCAGTGTAGAGGTGACCTTGCCCTTAATATATTTGTGAAGTTAAAATTTTAAAGA
TAGCTCATGAACTTTTGTCTAAGCAAAAAGAAAACCTCGAATTGAAATGTGTGAGGCAAACTATGCATGGGAAT
AGCTTAATGTGAAGATAATCATTTGGACAACCTCAAATCCATCAACATGACCAATGTTTTTTCATCTGCCACATCTC
AAAAATAAACTTCTGGTGAAACAAATTAAACAAAATATCCAAACCTCAAAAAAA

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FIGURE 278

MKTFTWTLGVLFLLVDTGHCRRGGQFKIKKINQRRYP RATDGKEEAKKCAYTFLVPEQRITGP
ICVNTKGQDASTIKDMITRMDLENLKDVL SRQKREIDVLQLVVDVDGNIVNEVKLLRKESRNM
NSRVTQLYMQLLHEIIRKRDNSLELSQLENKILNVTTEMLKMATRYRELEVKYASLTDLVNNQ
SVMITLLEEQCLRIFSRQDTHVSPPLVQVVPQHIPNSQQYTPG LLGGNEIQRDPGYPRDLMP P
PDLATSPTKSPFKIPPVTFINEGPFKDCQQA KEAGHSVSGIYMIKPENSNGPMQLWCENSLDP
GGWTVIQKRTDGSVNFFRNWENYKKGFGNIDGEYWLGLENIYMLSNQDNYKLLIELEDWSDKK
VYAEYSSFRLEPESEFYRLRLGTYQGNAGDSMMWHNGKQFTTLDRDKDMYAGNCAHFHKGGWW
YNACAHSNLNGVWYRGGHYRSKHQDGI FWA EYRGGSYSLRAVQMMIKPID

Important features:**Signal sequence:**

Amino acids 1-23

N-glycosylation sites:

Amino acids 160-164;188-192

cAMP- and cGMP-dependent protein kinase phosphorylation site:

Amino acids 120-124

Tyrosine kinase phosphorylation sites:

Amino acids 173-180;387-396

N-myristoylation sites:Amino acids 70-76;110-116;232-238,343-349;400-406;467-473;
475-487**Fibrinogen beta and gamma chains C-terminal domain signature:**

Amino acids 440-453

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FIGURE 279

CCCACGCGTCCGCGCAGTCGCGCAGTTCTGCCTCCGCCTGCCAGTCTCGCCCGCGATCCCGGC
CCGGGGCTGTGGCGTCGACTCCGACCCAGGCAGCCAGCAGCCCGCGCGGGAGCCGGACCGCCG
CCGGAGGAGCTCGGACGGCATGCTGAGCCCCCTCCTTTGCTGAAGCCCGAGTGCGGAGAAGCC
CGGGCAAACGCAGGCTAAGGAGACCAAAGCGGGCGAAGTCGCGAGACAGCGGACAAGCAGCGGA
GGAGAAGGAGGAGGAGGCGAACCCAGAGAGGGGCAGCAAAAGAAGCGGTGGTGGTGGGCGTCG
TGGCCATGGCGGGCGGCTATCGCCAGCTCGCTCATCCGTCAGAAGAGGCAAGCCCGCGAGCGCG
AGAAATCCAACGCCTGCAAGTGTGTGAGCAGCCCCAGCAAAGGCAAGACCAGCTGCGACAAAA
ACAAGTTAAATGTCTTTTCCCGGGTCAAACCTCTTCGGCTCCAAGAAGAGGCGCAGAAGAAGAC
CAGAGCCTCAGCTTAAGGGTATAGTTACCAAGCTATACAGCCGACAAGGCTACCACTTGCAGC
TGCAGGCGGATGGAACCATTTGATGGCACCAAAGATGAGGACAGCACTTACACTCTGTTTAACC
TCATCCCTGTGGGTCTGCGAGTGGTGGCTATCCAAGGAGTTCAAACCAAGCTGTACTTGGCAA
TGAACAGTGAGGGATACTTGTACACCTCGGAACTTTTCACACCTGAGTGCAAATTCAAAGAAT
CAGTGTTTGAAAATTATTATGTGACATATTCATCAATGATATACCGTCAGCAGCAGTCAGGCC
GAGGGTGGTATCTGGGTCTGAACAAAGAAGGAGAGATCATGAAAGGCAACCATGTGAAGAAGA
ACAAGCCTGCAGCTCATTTTCTGCCTAAACCACTGAAAGTGGCCATGTACAAGGAGCCATCAC
TGCACGATCTCACGGAGTTCTCCCGATCTGGAAGCGGGACCCCAACCAAGAGCAGAAGTGTCT
CTGGCGTGCTGAACGGAGGCAAATCCATGAGCCACAATGAATCAACGTAGCCAGTGAGGGCAA
AAGAAGGGCTCTGTAACAGAACCTTACCTCCAGGTGCTGTTGAATTCTTCTAGCAGTCCTTCA
CCCAAAGTTCAAATTTGTCAGTGACATTTACCAAACAAACAGGCAGAGTTCACTATTCTATC
TGCCATTAGACCTTCTTATCATCCATACTAAAGC

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FIGURE 280

MAAAIASSLIRQKRQAREREKSNACKCVSSPSKGKTSCDKNKLNVFSRVKLFSGSKKRRRRRPE
PQLKGIIVTKLYSRQGYHLQLQADGTIDGTDKDEDSTYTLFNLI PVGLRVVAIQGVQTKLYLAMN
SEGLYLTSELFTPECKFKESVFENYYVTYSSMIYRQQQSGRGWYLGLNKEGEIMKGNHVKKNK
PAAHFLPKPLKVAMYKEPSLHDLTEFSRSGSGTPTKSRSVSGVLNGGKSMSHNEST

Important Features:**N-glycosylation site:**

Amino acids 242-246

Glycosaminoglycan attachment sites:

Amino acids 165-169, 218-222

Tyrosine kinase phosphorylation site:

Amino acids 93-100

N-myristoylation sites:

Amino acids 87-93, 231-237

ATP/GTP-binding site motif A (P-loop):

Amino acids 231-239

HBGF/FGF family proteins:

Amino acids 78-94, 102-153

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FIGURE 281

CCAGGATGGAGCTGGGGCCTGTATAGCCATATTATTGTTCTATGCTACTAGACATGGGGGGGA
CTTGGTGAAAAAGGTATTATCCAGCCAGAGGGTCTGGGAGCCCTGTCTTACTGAACCTGGGCA
ACCTGGATATTCTGAGACATATTTTGGGGGGATTTTCAGTGAAAAAAGTGGGGGATCCCCTCCA
TTTAGAGTGTAGCAAAGGAAAAAACACCAAGGTTGGGTTCCCTTCCTGACATTGGCAGTGCCCC
AGTAGGGGTGGGATGAGCGAATATTCCTCAAAGCTAAAGTCCCACACCCTGTAGATTACAAGAG
TGGATTTGGCAGGAGTGTGCCCCAAAATACAGTGGAAAGGTGCCTGAAGATATTTAAACCACG
TCTTGGAAATTTAGTGGGTCTTGGCTTTGGGATAGGTGAAGTGAGGACAGACACTGGAGAGGA
GGGAAAGGGGACGTTTTTCAATAGGAGGCAAACTCGAGGGTGGGATCCACTGAGGAGTACATA
GGCTGCTGGATCTGGTGGAGCCAGCACTGGGCCCCACGGGTGGTAACTGGCTGCTGTGGAGGGG
GGTACGTGAGGGGGGGGTCTGGGGCTTATCCTCAGGTCCTGTGGGTGGGGCAGCGAGTCGGGG
CCTGAGCGTCAAGAGCATGCCCTAGTGAGCGGGCTCCTCTGGGGGAGCCCAGCGCGCTCCGGG
CGCCTGCCGGTTTTGGGGGTGTCTCCTCCCGGGGCGCT**ATG**GCGGCGCTGGCCAGTAGCCTGAT
CCGGCAGAAGCGGGAGGTCCGCGAGCCCGGGGGCAGCCGGCCGGTGTGCGCGCAGCGGCGCGT
GTGTCCCCGCGGCACCAAGTCCCTTTGCCAGAAGCAGCTCCTCATCCTGCTGTCCAAGGTGCG
ACTGTGCGGGGGGCGGCCCCGCGCGGCCGGACCGCGGGCCGGAGCCTCAGCTCAAAGGCATCGT
CACCAAACGTGTTCTGCCGCCAGGGTTTCTACCTCCAGGCGAATCCCGACGGAAGCATCCAGGG
CACCCCAGAGGATACCAGCTCCTTCACCCACTTCAACCTGATCCCTGTGGGCCTCCGTGTGGT
CACCATCCAGAGCGCCAAGCTGGGTCACTACATGGCCATGAATGCTGAGGGACTGCTCTACAG
TTCGCCGCATTTACAGCTGAGTGTCGCTTTAAGGAGTGTGTCTTTGAGAATTACTACGTCCT
GTACGCCTCTGCTCTCTACCGCCAGCGTCGTTCTGGCCGGGCCTGGTACCTCGGCCTGGACAA
GGAGGGCCAGGTCATGAAGGGAAACCGAGTTAAGAAGACCAAGGCAGCTGCCCACTTTCTGCC
CAAGCTCCTGGAGGTGGCCATGTACCAGGAGCCTTCTCTCCACAGTGTCCCCGAGGCCTCCCC
TTCCAGTCCCCCTGCCCCC**TGA**AATGTAGTCCCTGGACTGGAGGTTCCCTGCACTCCCAGTGA
GCCAGCCACCACCAACCTGT

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FIGURE 282

MAALASSLIRQKREVPGGSRPVSAQRRVCPRGTKSLCQKQLLILLSKVRLCGGRPARPDRG
PEPQLKGIIVTKLFCRQGFFYLQANPDGSIQGTPEDTSSFTFHNLI PVGLRVVTIQSAKLGHYMA
MNAEGLLYSSPHFTAECRFKECVFENYYVLYASALYRQRRSGRAWYLGLDKEGQVMKGNRVKK
TKAAAHFLPKLLEVAMYQEPSLHSVPEASPSPPAP

Important features:**Tyrosine kinase phosphorylation site:**

Amino acids 199-207

N-myristoylation sites:

Amino acids 54-60; 89-95; 131-137

HBGF/FGF family signature:

Amino acids 131-155

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FIGURE 283

ATGCCCGCGGCCATCGCTAGCGGCTTGATCCGCCAGAAGCGGCAGGCGCGGGAGCAGCACTGG
GACCGGCCGTCTGCCAGCAGGAGGCGGAGCAGCCCCAGCAAGAACCGCGGGGCTCTGCAACGGC
AACCTGGTGGATATCTTCTCCAAAGTGCGCATCTTCGGCCTCAAGAAGCGCAGGTTGCGGCGC
CAAGATCCCCAGCTCAAGGGTATAGTGACCAGGTTATATTGCAGGCAAGGCTACTACTTGCAA
ATGCACCCCGATGGAGCTCTCGATGGAACCAAGGATGACAGCACTAATTCTACACTCTTCAAC
CTCATACCAGTGGGACTACGTGTTGTTGCCATCCAGGGAGTGAAAACAGGGTTGTATATAGCC
ATGAATGGAGAAGGTTACCTCTACCCATCAGAACTTTTTACCCCTGAATGCAAGTTTAAAGAA
TCTGTTTTTTGAAAATTATTATGTAATCTACTCATCCATGTTGTACAGACAACAGGAATCTGGT
AGAGCCTGGTTTTTTGGGATTAAATAAGGAAGGGCAAGCTATGAAAGGGAACAGAGTAAAGAAA
ACCAAACCAGCAGCTCATTTTCTACCCAAGCCATTGGAAGTTGCCATGTACCGAGAACCATCT
TTGCATGATGTTGGGGAAACGGTCCCGAAGCCTGGGGTGACGCCAAGTAAAAGCACAAGTGCG
TCTGCAATAATGAATGGAGGCAAACAGTCAACAAGAGTAAGACAACA**TAG**

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FIGURE 284

MAAAIASGLIRQKRQAREQHWDRPSASRRRSSPSKNRGLCNGNLVDIFSKVRI FGLKKRRLRR
QDPQLKGIVTRLYCRQGYYLQMHPDGALDGTKDDSTNSTLFNLI PVGLRVVAIQGVKTGLYIA
MNGEGYLYPSELF TPECKFKESVFENYYVIYSSMLYRQQESGRAWFLGLNKEGQAMKGNRVKK
TKPAAHFLPKPLEVAMYREPSLHDVGETVPKPGVTPSKSTSASAIMNGGKPVNKS KTT

Important features:**N-glycosylation sites:**

Amino acids 100-104, 242-246

cAMP- and cGMP-dependent protein kinase phosphorylation sites:

Amino acids 28-32, 29-33

Tyrosine kinase phosphorylation site:

Amino acids 199-207

N-myristoylation sites:

Amino acids 38-44, 89-95, 118-124, 122-128, 222-228

HBGF/FGF family proteins:

Amino acids 104-155, 171-198

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FIGURE 285

CGGACGCGTGGGCGGACGCGTGGGCGGACGCGTGGGCGGACGCGTGGGCTGGTTCAGGTCCAGGTTTTGCTTTGA
TCCTTTTCAAAAACTGGAGACACAGAAGAGGGCTCTAGGAAAAAGTTTTGGATGGGATTATGTGGAACTACCCT
GCGATTCTCTGCTGCCAGAGCAGGCTCGGCGCTTCCACCCAGTGCAGCCTTCCCCTGGCGGTGGTGAAAGAGAC
TCGGGAGTCGCTGCTTCCAAAGTGCCCGCCGTGAGTGAGCTCTCACCCAGTGCAGCCAAATGAGCCTCTTCGGGC
TTCTCCTGCTGACATCTGCCCTGGCCGGCCAGAGACAGGGGACTCAGGCGGAATCCAACCTGAGTAGTAAATTCC
AGTTTTCCAGCAACAAGGAACAGAACGGAGTACAAGATCCTCAGCATGAGAGAATTATTACTGTGTCTACTAATG
GAAGTATTCACAGCCCAAGGTTTCTCATACTTATCCAAGAAATACGGTCTTGGTATGGAGATTAGTAGCAGTAG
AGGAAAATGTATGGATACAACCTTACGTTTGATGAAAGATTTGGGCTTGAAGACCAGAAGATGACATATGCAAGT
ATGATTTTGTAGAAGTTGAGGAACCCAGTGATGGAATATATTAGGGCGCTGGTGTGGTTCTGGTACTGTACCAG
GAAAACAGATTTCTAAAGGAAATCAAATTAGGATAAGATTTGTATCTGATGAATATTTTCTTCTGAACCAGGGT
TCTGCATCCACTACAACATTGTCTATGCCACAATTACAGAAAGCTGTGAGTCCTTCAGTGCTACCCCTTCAGCTT
TGCCACTGGACCTGCTTAATAATGCTATAACTGCCTTTAGTACCTTGAAGACCTTATTGATATCTTGAACCAG
AGAGATGGCAGTTGGACTTAGAAGATCTATATAGGCCAACTTGGCAACTTCTTGGCAAGGCTTTTGTTTTTGGAA
GAAAATCCAGAGTGGTGGATCTGAACCTTCTAACAGAGGAGGTAAGATTATACAGCTGCACACCTCGTAACCTCT
CAGTGTCATAAGGGAAGAACTAAAGAGAACCGATACCATTTTCTGGCCAGGTTGTCTCCTGGTTAAACGCTGTG
GTGGGAACTGTGCCTGTTGTCTCCACAATTGCAATGAATGTCAATGTGTCCCAAGCAAAGTTACTAAAAAATACC
ACGAGGTCTTTCAGTTGAGACCAAAGACCGGTGTCAGGGGATTGCACAAATCACTCACCGACGTGGCCCTGGAGC
ACCATGAGGAGTGTGACTGTGTGTGCAGAGGGAGCACAGGAGGATAGCCGCATCACCACCAGCAGCTCTTGCCCA
GAGCTGTGCAGTGCAGTGGCTGATTCTATTAGAGAACGTATGCGTTATCTCCATCCTTAATCTCAGTTGTTTGCT
TCAAGGACCTTTCATCTTCAGGATTTACAGTGCATTCTGAAAGAGGAGACATCAAACAGAATTAGGAGTTGTGCA
ACAGCTCTTTTGAGAGGAGGCCATAAGGACAGGAGAAAAAGGTCTTCAATCGTGGAAAGAAAATTAAATGTTGTAT
TAAATAGATCACCAGCTAGTTTCAGAGTTACCATGTACGTATTCCTACTAGCTGGGTTCTGTATTTTCAGTTCTTTC
GATACGGCTTAGGGTAATGTCAGTACAGGAAAAAACTGTGCAAGTGAGCACCTGATTCCGTTGCCTTGCTTAAC
TCTAAAGCTCCATGTCCTGGGCCTAAATCGTATAAAATCTGGATTTTTTTTTTTTTTTTTTGTCTCATATTCACAT
ATGTAAACCAGAACATTCTATGTACTACAAACCTGGTTTTTAAAAAGGAACTATGTTGCTATGAATTAACCTTGT
GTCATGCTGATAGGACAGACTGGATTTTTTCATATTTCTTATTAAATTTCTGCCATTTAGAAGAAGAGAACTACA
TTCATGGTTTGGAAAGAGATAAACCTGAAAAGAAGAGTGGCCTTATCTTCACTTTATCGATAAGTCAGTTTATTTG
TTTCATTGTGTACATTTTTATATTCTCCTTTTGACATTATAACTGTTGGCTTTTCTAATCTTGTTAAATATATCT
ATTTTTACCAAAGGTATTTAATATTCTTTTTTATGACAACTTAGATCAACTATTTTTAGCTTGGTAAATTTTTCT
AAACACAATTGTTATAGCCAGAGGAACAAAGATGATATAAAATATTGTTGCTCTGACAAAAATACATGATTTCA
TTCTCGTATGGTGCTAGAGTTAGATTAATCTGCATTTTAAAAAACTGAATTGGAATAGAATTGGTAAGTTGCAAA
GACTTTTTGAAAATAATTAAATTATCATATCTTCCATTCTGTTATTGGAGATGAAAATAAAAAGCAACTTATGA
AAGTAGACATTGATCCAGCCATTACTAACCTATTCTTTTTTGGGGAAATCTGAGCCTAGCTCAGAAAAACAT
AAAGCACCTTGAAAAAGACTTGGCAGCTTCCTGATAAAGCGTGCTGTGCTGTGCAGTAGGAACACATCCTATTTA
TTGTGATGTTGTGGTTTTATTATCTTAAACTCTGTTCCATACACTTGTATAAATACATGGATATTTTTATGTACA
GAAGTATGTCTCTTAACAGTTCACCTATTGTACTCTGGCAATTTAAAGAAAATCAGTAAAATATTTTGCTTGT
AAAATGCTTAATATNGTGCCTAGGTTATGTGGTGACTATTTGAATCAAAAATGTATTGAATCATCAAAATAAAGA
ATGTGGCTATTTTGGGGAGAAAATTAAAAAAGGTTTAGGGATAACAGGGTAATGCGGCC

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FIGURE 286

MSLFGLLLLT SALAGQRQGTQAESNLSSKFQFSSNKEQNGVQDPQHERIITVSTNGSIHSPRF
PHTYPRNTVLVWRLVAVEENVWIQLTDFDERFGLEDPEDDICKYDFVEVEEPSDGTILGRWCGS
GTVPGKQISKGNQIRIRFVSDEYFPSEPGFCIHYNIVMPQFTEAVSPSVLPPSALPLDLLNNA
ITAFSTLEDLIRYLEPERWQLDLEDLYRPTWQLLGKAFVFGRKSRVVDLNLLEEVRLYSCTP
RNFSVSIREELKRTDTIFWPGCLLVKRCGGNCACCLHNCNECQCVPSKVTKKYHEVLQLRPKT
GVRGLHKSLTDVALEHHEECDVCVRGSTGG

Important features:**signal sequence:**

Amino acids 1-14

N-glycosylation sites:

Amino acids 25-29;55-59;254-258

N-myristoylation sites:

Amino acids 15-21;117-123;127-133;281-287;282-288;319-325

Amidation site:

Amino acids 229-233

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FIGURE 287

CAGCGCTGACTGCGCCGCGGAGAAAGCCAGTGGGAACCCAGACCCATAGGAGACCCGCGTCCC
CGCTCGGCCTGGCCAGGCCCCGCGCT**ATG**GAGTTCCTCTGGGCCCCCTCTCTTGGGTCTGTGCT
GCAGTCTGGCCGCTGCTGATCGCCACACCGTCTTCTGGAACAGTTCAAATCCCAAGTTCCGGA
ATGAGGACTACACCATACATGTGCAGCTGAATGACTACGTGGACATCATCTGTCCGCACTATG
AAGATCACTCTGTGGCAGACGCTGCCATGGAGCAGTACATACTGTACCTGGTGGAGCATGAGG
AGTACCAGCTGTGCCAGCCCCAGTCCAAGGACCAAGTCCGCTGGCAGTGCAACCGGCCAGTG
CCAAGCATGGCCCCGGAGAAGCTGTCTGAGAAGTTCCAGCGCTTCACACCTTTCACCCTGGGCA
AGGAGTTCAAAGAAGGACACAGCTACTACTACATCTCCAAACCCATCCACCAGCATGAAGACC
GCTGCTTGAGGTTGAAGGTGACTGTCAGTGGCAAAATCACTCACAGTCCTCAGGCCCCATGACA
ATCCACAGGAGAAGAGACTTGCAGCAGATGACCCAGAGGTGCGGGTTCTACATAGCATCGGTC
ACAGTGCTGCCCCACGCCTCTTCCCACTTGCCTGGACTGTGCTGCTCCTTCCACTTCTGCTGC
TGCAAACCCCG**TGA**AGGTGTGTGCCACACCTGGCCTTAAAGAGGGACAGGCTGAAGAGAGGGA
CAGGCACTCCAAACCTGTCTTGGGGCCACTTTCAGAGCCCCCAGCCCTGGGAACCACTCCCAC
CACAGGCATAAGCTATCACCTAGCAGCCTCAAAACGGGTCAATATTAAGGTTTTCAACCGGAA
GGAGGCCAACCAGCCCGACAGTGCCATCCCCACCTTCACCTCGGAGGGATGGAGAAAGAAGTG
GAGACAGTCCTTTCCCACCATTCCTGCCTTTAAGCCAAAGAAACAAGCTGTGCAGGCATGGTC
CCTTAAGGCACAGTGGGAGCTGAGCTGGAAGGGGCCACGTGGATGGGCAAAGCTTGTCAAAGA
TGCCCCCTTCAGGAGAGAGCCAGGATGCCCAGATGAACTGACTGAAGGAAAAGCAAGAAACAG
TTTCTTGCTTGGAAGCCAGGTACAGGAGAGGCAGCATGCTTGGGCTGACCCAGCATCTCCCAG
CAAGACCTCATCTGTGGAGCTGCCACAGAGAAGTTTGTAGCCAGGTACTGCATTCTCTCCCAT
CCTGGGGCAGCACTCCCCAGAGCTGTGCCAGCAGGGGGGCTGTGCCAACCTGTTCTTAGAGTG
TAGCTGTAAGGGCAGTGCCCATGTGTACATTCTGCCTAGAGTGTAGCCTAAAGGGCAGGGCCC
ACGTGTATAGTATCTGTATATAAGTTGCTGTGTGTCTGTCCTGATTTCTACAACCTGGAGTTTT
TTTATACAATGTTCTTTGTCTCAAAATAAAGCAATGTGTTTTTTTCGG

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FIGURE 288

MEFLWAPLLGLCCSLAAADRHTVFWNSSNPKFRNEDYTIHVQLNDYVDIICPHYEDHSADAAM
EQYILYLVEHEEYQLCQPQSKDQVRWQCNRPQSAKHGPEKLSEKFQRFPTPFTLGKEFKEGHSYY
YISKPIHQHEDRCLRLKVTVSGKITHSPQAHDNPQEKRLAADDPEVRVLHSIGHSAAPRLFPL
AWTVLLLPLLLLQTP

Important features:**Signal sequence:**

Amino acids 1-17

N-glycosylation site:

Amino acids 26-30

Tyrosine kinase phosphorylation site:

Amino acids 118-127

N-myristoylation site:

Amino acids 10-16

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FIGURE 289

CGGACGCGTGGGCGGACGCGTGGGCGGCCACGGCGCCCGCGGGCTGGGGCGGTGCGTTCTTC
CTTCTCCGTGGCCTACGAGGGTCCCCAGCCTGGGTAAAGATGGCCCCATGGCCCCGAAGGGC
CTAGTCCCAGCTGTGCTCTGGGGCCTCAGCCTCTTCCTCAACCTCCCAGGACCTATCTGGCTC
CAGCCCTCTCCACCTCCCCAGTCTTCTCCCCCGCCTCAGCCCCATCCGTGTCATACCTGCCGG
GGA CTGGTTGACAGCTTTAACAAGGGCCTGGAGAGAACCATCCGGGACAACCTTTGGAGGTGGA
AACTGCTGGGAGGAAGAGAATTTGTCAAATACAAAGACAGTGAGACCCGCCTGGTAGAG
GTGCTGGAGGGTGTGTGCAGCAAGTCAGACTTCGAGTGCCACCGCCTGCTGGAGCTGAGTGAG
GAGCTGGTGGAGAGCTGGTGGTTTCACAAGCAGCAGGAGGCCCCGGACCTCTTCCAGTGGCTG
TGCTCAGATTCCCTGAAGCTCTGCTGCCCCGCAGGCACCTTCGGGGCCCTCCTGCCTTCCCTGT
CCTGGGGGAACAGAGAGGGCCCTGCGGTGGCTACGGGCAGTGTGAAGGAGAAGGGACACGAGGG
GGCAGCGGGCACTGTGACTGCCAAGCCGGCTACGGGGGTGAGGCCTGTGGCCAGTGTGGCCTT
GGCTACTTTGAGGCAGAACGCAACGCCAGCCATCTGGTATGTTTCGGCTTGTTTTGGCCCCCTGT
GCCCGATGCTCAGGACCTGAGGAATCAAACCTGTTTGCAATGCAAGAAGGGCTGGGCCCTGCAT
CACCTCAAGTGTGTAGACATTGATGAGTGTGGCACAGAGGGAGCCAACCTGTGGAGCTGACCAA
TTCTGCGTGAACACTGAGGGCTCCTATGAGTGCCGAGACTGTGCCAAGGCCTGCCTAGGCTGC
ATGGGGGCAGGGCCAGGTCGCTGTAAGAAGTGTAGCCCTGGCTATCAGCAGGTGGGCTCCAAG
TGTCTCGATGTGGATGAGTGTGAGACAGAGGTGTGTCCGGGAGAGAAACAAGCAGTGTGAAAAC
ACCGAGGGCGGTTATCGCTGCATCTGTGCCGAGGGCTACAAGCAGATGGAAGGCATCTGTGTG
AAGGAGCAGATCCCAGAGTCAGCAGGCTTCTTCTCAGAGATGACAGAAGACGAGTTGGTGGTG
CTGCAGCAGATGTTCTTTGGCATCATCATCTGTGCACTGGCCACGCTGGCTGCTAAGGGCGAC
TTGGTGTTACCGCCATCTTCATTGGGGCTGTGGCGGCCATGACTGGCTACTGGTTGTGAGAG
CGCAGTGACCGTGTGCTGGAGGGCTTCATCAAGGGCAGATTAATCGCGGCCACCACCTGTAGGA
CCTCCTCCCACCCACGCTGCCCCAGAGCTTGGGCTGCCCTCCTGCTGGACACTCAGGACAGC
TTGGTTTATTTTTGAGAGTGGGGTAAGCACCCCTACCTGCCTTACAGAGCAGCCCAGGTACCC
AGGCCCGGGCAGACAAGGCCCTGGGGTAAAAAGTAGCCCTGAAGGTGGATAACCATGAGCTCT
TCACCTGGCGGGGACTGGCAGGCTTCACAATGTGTGAATTTCAAAGTTTTTCCTTAATGGTG
GCTGCTAGAGCTTTGGCCCCCTGCTTAGGATTAGGTGGTCCTCACAGGGGTGGGGCCATCACAG
CTCCCTCCTGCCAGCTGCATGCTGCCAGTTCCTGTTCTGTGTTACCCACATCCCCACACCCCA
TTGCCACTTATTTATTCATCTCAGGAAATAAAGAAAGGTCTTGAAAGTTAAAAAAAAAAAAA
AAAAAAAAAAAA

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FIGURE 290

MAPWPPKGLVPAVLWGLSLFLNLP GPIWLQPSPPPQSSPPPQPHPCHTCRGLVDSFNKGLERT
IRDNFGGGNTAWEENLSKYKDSETRLVEVLEGVCSKSDFECHRLLELSEELVESWWFHKQQE
APDLFQWLCSDSLKLCCPAGTFGPSCLPCPGGTERPCGGYGQCEGEGTRGGSGHCDCQAGYGG
EACGQCGLGYFEAERNASHLVCSACFGPCARCSGPEESNCLQCKKGWALHHLKCVDIDECGTE
GANCGADQFCVNTEGSYECRDCAKACLGCMGAGPGRCKKCSPGYQQVGSKCLDVDECETEVCP
GENKQCENTEGGYRCICAEGYKQMEGICVKEQIPESAGFFSEMTEDLVVLQQMFFGIICAL
ATLAAKGDVFTAIFIGAVAAMTGYWLSERSDRVLEGFIKGR

Important features:**Signal sequence:**

Amino acids 1-29

Transmembrane domain:

Amino acids 342-392

N-glycosylation sites:

Amino acids 79-83;205-209

cAMP- and cGMP-dependent protein kinase phosphorylation site:

Amino acids 290-294

Aspartic acid and asparagine hydroxylation site:

Amino acids 321-333

EGF-like domain cysteine pattern signature:

Amino acids 181-193

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FIGURE 291

CAGGTCCAACCTGCACCTCGGTTCTATCGATTGAATTCCCCGGGGATCCTCTAGAGATCCCTCGACCTCGACCCAC
GCGTCCGAACACAGGTCCTTGTTGCTGCAGAGAAGCAGTTGTTTTGCTGGAAGGAGGGAGTGCGCGGGCTGCCCC
GGGCTCCTCCCTGCCGCCTCCTCTCAGTGGATGGTTCCAGGCACCCCTGTCTGGGGCAGGGAGGGCACAGGCCTGC
ACATCGAAGGTGGGGTGGGACCAGGCTGCCCCCTCGCCCCAGCATCCAAGTCCTCCCTTGGGCGCCCGTGGCCCTG
CAGACTCTCAGGGCTAAGGTCTCTGTTGCTTTTTGGTTCCACCTTAGAAGAGGCTCCGCTTGACTAAGAGTAGC
TTGAAGGAGGCACCAATGCAGGAGCTGCATCTGCTCTGGTGGGCGCTTCTCCTGGGCCTGGCTCAGGCCTGCCCTG
AGCCCTGCGACTGTGGGGAAAAGTATGGCTTCCAGATCGCCGACTGTGCCTACCGCGACCTAGAATCCGTGCCGC
CTGGCTTCCCGGCCAATGTGACTACACTGAGCCTGTGAGCCAAACGGGCTGCCAGGCTTGCCGGAGGGTGCCCTCA
GGGAGGTGCCCCCTGCTGCAGTCGCTGTGGCTGGCACACAATGAGATCCGCACGGTGGCCGCCGGAGCCCTGGCCT
CTCTGAGCCATCTCAAGAGCCTGGACCTCAGCCACAATCTCATCTCTGACTTTGCCTGGAGCGACCTGCACAACC
TCAGTGCCCTCCAATTGCTCAAGATGGACAGCAACGAGCTGACCTTCATCCCCGCGACGCCTTCCGCAGCCTCC
GTGCTCTGCGCTCGCTGCAACTCAACCACAACCGCTTGACACATTGGCCGAGGGCACCTTACCCCCGCTCACCG
CGCTGTCCCACCTGCAGATCAACGAGAACCCCTTCGACTGCACCTGCGGCATCGTGTGGCTCAAGACATGGGCCC
TGACCACGGCCGTGTCCATCCCGGAGCAGGACAACATCGCCTGCACCTCACCCCATGTGCTCAAGGGTACACCGC
TGAGCCGCCTGCCGCCACTGCCATGCTCGGCGCCCTCAGTGCAGCTCAGCTACCAACCCAGCCAGGATGGTGCCG
AGCTGCGGCCTGGTTTTGTGCTGGCACTGCACTGTGATGTGGACGGGCAGCCGGCCCCCTCAGCTTCACTGGCACA
TCCAGATACCCAGTGGCATTTGTGGAGATCACCAGCCCCAACGTGGGCACCTGATGGGCGTGCCCTGCCCTGGCACCC
CTGTGGCCAGCTCCCAGCCGCGCTTCCAGGCCTTTGCCAATGGCAGCCTGCTTATCCCCGACTTTGGCAAGCTGG
AGGAAGGCACCTACAGCTGCCTGGCCACCAATGAGCTGGGCAGTGTGAGAGCTCAGTGGACGTGGCACTGGCCA
CGCCCCGTGAGGGTGGTGAGGACACACTGGGGCGCAGGTTCCATGGCAAAGCGTTGAGGGAAAGGGCTGCTATA
CGGTTGACAACGAGGTGCAGCCATCAGGGCCGGAGGACAATGTGGTCATCATCTACCTCAGCCGTGCTGGGAACC
CTGAGGCTGCAGTCGCAGAAGGGGTCCCTGGGCAGCTGCCCCCAGGCCTGCTCCTGCTGGGCCAAAGCCTCCTCC
TCTTCTTCTTCTCCTCACCTCCTTCAGCCCCACCCAGGGCTTCCCTAACTCCTCCCCTTGCCCCCTACCAATGCCCC
TTTAAGTGCTGCAGGGGTCTGGGGTTGGCAACTCCTGAGGCCTGCATGGGTGACTTCACATTTTCTACCTCTCC
TTCTAATCTCTTCTAGAGCAGCTGCTATCCCCAATTCTAGACCTGCTCCAACTAGTGACTAGGATAGAATTTG
ATCCCCTAACTCACTGTCTGCGGTGCTCATTGCTGCTAACAGCATTGCCTGTGCTCTCCTCTCAGGGGCAGCATG
CTAACGGGGCGACGTCTAATCCAATGGGAGAAGCCTCAGTGGTGGAATTCCAGGCACTGTGACTGTCAAGCTG
GCAAGGGCCAGGATTGGGGGAATGGAGCTGGGGCTTAGCTGGGAGGTGGTCTGAAGCAGACAGGGAATGGGAGAG
GAGGATGGGAAGTAGACAGTGGCTGGTATGGCTCTGAGGCTCCCTGGGGCCTGCTCAAGCTCCTCCTGCTCCTTG
CTGTTTTCTGATGATTTGGGGGCTTGGGAGTCCCTTTGTCTCATCTGAGACTGAAATGTGGGGATCCAGGATGG
CCTTCCTTCTTCTTACCCTTCTCCCTCAGCCTGCAACCTCTATCCTGGAACCTGTCTCCTTTCTCCCCAACT
ATGCATCTGTTGTCTGCTCCTCTGCAAAGGCCAGCCAGCTTGGGAGCAGCAGAGAAATAAACAGCATTTCTGATG
CCAAAAAAGGGCGGCCGCGACTCTAGAGTCGACCT

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FIGURE 292

MQELHLLWWALLLGLAQACPEPCDCGEKYGFQIADCAYRDLESVPPGFANVTTLSSLNRLP
GLPEGAFREVPLLQSLWLAHNEIRTVAAGALASLSHLKSLDLSHNLISDFAWSDLHNLNLSALQL
LKMSNELTFIPRDAFRSLRALRSLQLNHNRLHTLAEGTFTPLTALSHLQINENPFDCCTCGIV
WLKTWALTAVSIPEQDNIACTSPHVLKGTPLSRLPPLPCSAAPSVQLSYQPSQDGAELRPGFV
LALHCDVDGQPAPQLHWHIQIPSGIVEITSPNVGTDGRALPGTPVASSQPRFQAFANGSLLIP
DFGKLEEGTYSCLATNELGSAESSVDVALATPGEGGEDTLGRRFHGKAVEGKGCYTVDNEVQP
SGPEDNVVIIYLSRAGNPEAAVAEGVPGQLPPGLLLLGQSLLLFFFLTSF

Important features:**Signal peptide:**

amino acids 1-18

Transmembrane domain:

amino acids 403-418

N-glycosylation sites:

Amino acids 51-55, 120-124, 309-313

Tyrosine kinase phosphorylation site:

amino acids 319-326

N-myristoylation sites:amino acids 14-20, 64-70, 92-98, 218-224, 294-300, 323-329, 334-340,
350-356, 394-400**Amidation site:**

amino acids 355-359

Leucine Rich Repeat:

amino acids 51-74, 75-98, 99-122, 123-146, 147-170

Leucine rich repeat C-terminal domain:

amino acids 180-230

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FIGURE 293

ACTTGGAGCAAGCGGCGGGCGGGGAGACAGAGGCAGAGGCAGAAGCTGGGGCTCCGTCTCGCCTCCCACGAGCG
ATCCCCGAGGAGAGCCGCGGCCCTCGGCGAGGCGAAGAGGCCGACGAGGAAGACCCGGGTGGCTGCGCCCCCTGCC
TCGCTTCCCAGGCGCCGGCGGGCTGCAGCCTTGCCCTCTTGCTCGCCTTGAAAATGGAAGAGATGCTCGCAGGCT
GCTTTCTGCTGATCCTCGGACAGATCGTCTCTCTCCCTGCCGAGGCCAGGGAGCGGTACAGTGGGAGGTCCATCT
CTAGGGGCGAGACACGCTCGGACCCACCCGCGAGACGGCCCTTCTGGAGAGTTCTGTGAGAACAAAGCGGGCAGACC
TGGTTTTTCATCATTGACAGCTCTCGCAGTGTCAACACCCATGACTATGCAAAGGTCAAGGAGTTCATCGTGGACA
TCTTGCAATTCTTGACATTGGTCTGATGTACCCGAGTGGGCCTGCTCCAATATGGCAGCACTGTCAAGAATG
AGTTCTCCCTCAAGACCTTCAAGAGGAAGTCCGAGGTGGAGCGTGTGTCAAGAGGATGCGGCATCTGTCCACGG
GCACCATGACTGGGCTGGCCATCCAGTATGCCCTGAACATCGCATTTCTCAGAAGCAGAGGGGGCCCGCCCCCTGA
GGGAGAATGTGCCACGGGTCAATATGATCGTGACAGATGGGAGACCTCAGGACTCCGTGGCCGAGGTGGCTGCTA
AGGCACGGGACACGGGCATCCTAATCTTTGCCATTGGTGTGGGCCAGGTAGACTTCAACACCTTGAAGTCCATTG
GGAGTGAGCCCCATGAGGACCATGTCTTCTTGTGGCCAATTTTCAGCCAGATTGAGACGCTGACCTCCGTGTTCC
AGAAGAAGTTGTGCACGGCCACATGTGCAGCACCTGGAGCATAACTGTGCCACTTCTGCATCAACATCCCTG
GCTCATACGTCTGCAGGTGCAAACAAGGCTACATTCTCAACTCGGATCAGACGACTTGCAGAATCCAGGATCTGT
GTGCCATGGAGGACCACAACCTGTGAGCAGCTCTGTGTGAATGTGCCGGGCTCCTTCGTCTGCCAGTGCTACAGTG
GCTACGCCCTGGCTGAGGATGGGAAGAGGTGTGTGGCTGTGGACTACTGTGCCTCAGAAAACACGGATGTGAAC
ATGAGTGTGTAATGCTGATGGCTCCTACCTTTGCCAGTGCCATGAAGGATTTGCTCTTAACCCAGATGAAAAAA
CGTGCACAAGGATCAACTACTGTGCACTGAACAAACCGGGCTGTGAGCATGAGTGCCTCAACATGGAGGAGAGCT
ACTACTGCCGCTGCCACCGTGGCTACACTCTGGACCCCAATGGCAAAACCTGCAGCCGAGTGGACCACTGTGCAC
AGCAGGACCATGGCTGTGAGCAGCTGTGTCTGAACACGGAGGATTCCTTCGTCTGCCAGTGCTCAGAAGGCTTCC
TCATCAACGAGGACCTCAAGACCTGCTCCCGGGTGGATTACTGCCTGCTGAGTGACCATGGTTGTGAATACTCCT
GTGTCAACATGGACAGATCCTTTGCCTGTCACTGTCTGAGGGACACGTGCTCCGCAGCGATGGGAAGACGTGTG
CAAAATTGGACTCTTGTGCTCTGGGGGACCACGGTTGTGAACATTCGTGTGTAAGCAGTGAAGATTTCGTTGTGT
GCCAGTGCTTTGAAGGTTATATACTCCGTGAAGATGGAAAAACCTGCAGAAGGAAGATGTCTGCCAAGCTATAG
ACCATGGCTGTGAACACATTTGTGTGAACAGTGACGACTCATACAGTGCGAGTGCTTGGAGGGATTCCGGCTCG
CTGAGGATGGGAAACGCTGCCGAAGGAAGGATGTCTGCAAATCAACCCACCATGGCTGCGAACACATTTGTGTTA
ATAATGGGAATTCCTACATCTGCAAATGCTCAGAGGGATTTGTTCTAGCTGAGGACGGAAGACGGTGCAAGAAAT
GCACTGAAGGCCCAATTGACCTGGTCTTTGTGATCGATGGATCCAAGAGTCTTGGAGAAGAGAATTTTGAGGTGCG
TGAAGCAGTTTGTCACTGGAATTATAGATTCCCTTGACAATTTCCCCCAAAGCCGCTCGAGTGGGGCTGCTCCAGT
ATTCACACAGGTCCACACAGAGTTCACCTCTGAGAACTTCAACTCAGCCAAAGACATGAAAAAGCCGTGGCCC
ACATGAAATACATGGGAAAGGGCTCTATGACTGGGCTGGCCCTGAAACACATGTTTGAGAGAAGTTTTACCCAAG
GAGAAGGGGCCAGGCCCTTTCCACAAGGGTGCCAGAGCAGCCATTGTGTTTACCGACGGACGGGCTCAGGATG
ACGTCTCCGAGTGGGCCAGTAAAGCCAAGGCCAATGGTATCACTATGTATGCTGTTGGGGTAGGAAAAGCCATTG
AGGAGGAACTACAAGAGATTGCCTCTGAGCCCAACAAACAAGCATCTCTTCTATGCCGAAGACTTCAGCACAATGG
ATGAGATAAGTAAAAAACTCAAGAAAGGCATCTGTGAAGCTCTAGAAGACTCCGATGGAAGACAGGACTCTCCAG
CAGGGGAACTGCCAAAAACGGTCCAACAGCCAACAGAATCTGAGCCAGTCACCATAAATATCCAAGACCTACTTT
CCTGTTCTAATTTTGCAGTGCAACACAGATATCTGTTTGAAGAAGACAATCTTTTACGGTCTACACAAAAGCTTT
CCCATTCAACAAAACCTTCAGGAAGCCCTTTGGAAGAAAAACACGATCAATGCAATGTGAAAACCTTATAATGT
TCCAGAACCTTGCAAACGAAGAAGTAAGAAAATTAACACAGCGCTTAGAAGAAATGACACAGAGAATGGAAGCCC
TGGAAAATCGCCTGAGATACAGATGAAGATTAGAAATCGCGACACATTTGTAGTCATTGTATCACGGATTACAAT
GAACGCAGTGCAGAGCCCCAAAGCTCAGGCTATTGTTAAATCAATAATGTTGTGAAGTAAAACAATCAGTACTGA
GAAACCTGGTTTGCCACAGAACAAGACAAGAAGTATACACTAACTTGTATAAATTTATCTAGGAAAAAAATCCT
TCAGAATTCTAAGATGAATTTACCAGGTGAGAATGAATAAGCTATGCAAGGTATTTTGTAAATATACTGTGGACAC
AACTTGCTTCTGCCTCATCTGCCTTAGTGTGCAATCTCATTGACTATACGATAAAGTTTTGCACAGTCTTACTT
CTGTAGAACACTGGCCATAGGAAATGCTGTTTTTTTGTACTGGACTTTACCTTGATATATGTATATGGATGTATG
CATAAATCATAGGACATATGTACTTGTGGAACAAGTTGGATTTTTTATACAATATTAAATTCACCACTTCAG

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FIGURE 294

MEKMLAGCFLILGQIVLLPAEARERSRGRSISRGRHARTHPTALLESSCENKRADLVFIID
SSRSVNTHDYAKVKEFIVDILQFLDIGPDVTRVGLLQYGSTVKNEFSCLKTFKRKSEVERAVKR
MRHLSTGTMGLAIQYALNIAFSEAEGARPLRENVPRVIMIVTDGRPQDSVAEVAAKARDTGI
LIFAIGVGQVDFNTLKSIGSEPHEDHVFLVANFSQIETLTSVFQKKLCTAHMCSTLEHNCAHF
CINIPGSYVCRCKQGYILNSDQTTTCRIQDLCAMEDHNCEQLCVNVPGSFVCQCYSYGYALAEDG
KRCVAVDYCASENHGCEHECVNADGSYLCQCHEGFALNPDEKTCTRINICALNKPGEHECVN
MEESYYCRCHRGYTLDPNGKTC SRVDHCAQQDHGCEQLCLNTEDSFVCQCSEGFLLINEDLKTC
SRVDYCLLSDHGCEYSCVNMDRSFACQCPGHLVLRSDGKTC AKLDSCALGDHGCEHSCVSSD
SFVCQCFEGYILREDGKTCRRKDVCQAIDHGCEHICVNSDDSYTCECLEGFRLAEDGKRCRRK
DVCKSTHHGCEHICVNNNGNSYICKCSEGFVLAEDGRRCKKCTEGPIDLVFVIDGSKSLGEENF
EVVKQFVTGIIDSLTISPKAARVGLLQYSTQVHTEFTLRNFNSAKDMKKAVAHMKYMGKGSMT
GLALKHMFERSFTQGEGARPLSTRVPRAAIVFTDGRAQDDVSEWASKAKANGITMYAVGVGKA
IEEELQEIASEPTNKHLYFAEDFSTMDEISEKLKKGICEALEDS DGRQDSPAGELPKTVQQPT
ESEPVTTINIQDLLSCSNFAVQHRYLFEEDNLLRSTQKLSHSTKPSGSPLEEKHDQCKCENLIM
FQNLANEEVRKLTQRLEEMTQRMEALENRLRYR

Important features:**Signal sequence:**

Amino acids 1-23

N-glycosylation site:

Amino acids 221-225

cAMP- and cGMP-dependent protein kinase phosphorylation sites:

Amino acids 115-119;606-610;892-896

N-myristoylation sites:Amino acids 133-139;258-264;299-305;340-346;453-459;494-500;
639-645;690-694;
752-758;792-798**Amidation sites:**

Amino acids 314-318;560-564;601-605

Aspartic acid and asparagine hydroxylation sites:Amino acids 253-265;294-306;335-347;376-388;417-429;
458-470;540-552;581-593

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FIGURE 295

GGCCGGAGCAGCACGGCCGCAGGACCTGGAGCTCCGGCTGCGTCTTCCCGCAGCGCTACCCGC
C**ATG**CGCCTGCCGCGCCGGGCCGCGCTGGGGCTCCTGCCGCTTCTGCTGCTGCTGCCGCCCGC
GCCGGAGGCCGCCAAGAAGCCGACGCCCTGCCACCGGTGCCGGGGGCTGGTGGACAAGTTTAA
CCAGGGGATGGTGGACACCGCAAAGAAGAACTTTGGCGGCGGGAACACGGCTTGGGAGGAAAA
GACGCTGTCCAAGTACGAGTCCAGCGAGATTTCGCCTGCTGGAGATCCTGGAGGGGCTGTGCGA
GAGCAGCGACTTCGAATGCAATCAGATGCTAGAGGCGCAGGAGGAGCACCTGGAGGCCTGGTG
GCTGCAGCTGAAGAGCGAATATCCTGACTTATTCGAGTGGTTTTGTGTGAAGACACTGAAAGT
GTGCTGCTCTCCAGGAACCTACGGTCCCGACTGTCTCGCATGCCAGGGCGGATCCCAGAGGCC
CTGCAGCGGGAATGGCCACTGCAGCGGAGATGGGAGCAGACAGGGCGACGGGTCCTGCCGGTG
CCACATGGGGTACCAGGGCCCGCTGTGCACTGACTGCATGGACGGCTACTTCAGCTCGCTCCG
GAACGAGACCCACAGCATCTGCACAGCCTGTGACGAGTCCTGCAAGACGTGCTCGGGCCTGAC
CAACAGAGACTGCGGCGAGTGTGAAGTGGGCTGGGTGCTGGACGAGGGCGCCTGTGTGGATGT
GGACGAGTGTGCGGCCGAGCCGCCTCCCTGCAGCGCTGCGCAGTTCTGTAAGAACGCCAACGG
CTCCTACACGTGCGAAGAGTGTGACTCCAGCTGTGTGGGCTGCACAGGGGAAGGCCCAGGAAA
CTGTAAAGAGTGTATCTCTGGCTACGCGAGGGAGCACGGACAGTGTGCAGATGTGGACGAGTG
CTCACTAGCAGAAAAAACCTGTGTGAGGAAAAACGAAAACCTGCTACAATACTCCAGGGAGCTA
CGTCTGTGTGTGTCCTGACGGCTTCGAAGAAACGGAAGATGCCTGTGTGCCGCCGGCAGAGGC
TGAAGCCACAGAAGGAGAAAGCCCGACACAGCTGCCCTCCCGCGAAGACCTG**TAA**TGTGCCGG
ACTTACCCTTTAAATTATTCAGAAGGATGTCCCGTGGAATGTGGCCCTGAGGATGCCGTCT
CCTGCAGTGGACAGCGGCGGGGAGAGGCTGCCTGCTCTTAACGGTTGATTCTCATTTGTCCC
TTAAACAGCTGCATTTCTTGGTTGTTCTTAAACAGACTTGATATTTTGATACAGTTCTTTGT
AATAAAATTGACCATTGTAGGTAATCAGGAGGAAAAAAAAA

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FIGURE 296

MRLPRRAALGLLPLLLLLPPAPEAAKKPTPCHRCRGLVDKFNQGMVDTAKKNFGGGNTAWEEK
TLSKYESSEIRLLEILEGLCESSDFECNQMLEAQEEHLEAWWLQLKSEYPDLFEWFCVKTLLKV
CCSPGTYGPDCLACQGGSQRPCSGNGHCSGDGSRQGDGSCRCHMGYQGPLCTDCMDGYFSSLR
NETHSICTACDESKTCSGLTNRDCGECEVGWVLDEGACVDVDECAAEPPPCSAAQFCKNANG
SYTCEECDSSCVGCTGEGPGNCKECISGYAREHGQCADVDECSLAEKTCVRKNENCYNTPGSY
VCVCPDGFEETEDACVPPAEAEATEGESPTQLPSREDL

Important features:**Signal peptide:**

Amino acids 1-24

N-glycosylation sites:

Amino acids 190-194;251-255

Glycosaminoglycan attachment sites:

Amino acids 149-153;155-159

cAMP- and cGMP-dependent protein kinase phosphorylation site:

Amino acids 26-30

Tyrosine kinase phosphorylation site:

Amino acids 303-310

N-myristoylation sites:Amino acids 44-50;54-60;55-61;81-87;150-156;158-164;164-170;
252-258;313-319**Aspartic acid and asparagine hydroxylation site:**

Amino acids 308-320

EGF-like domain cysteine pattern signature:

Amino acids 166-178

Leucine zipper pattern:

Amino acids 94-116

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FIGURE 297

GACATCGGAGGTGGGCTAGCACTGAACTGCTTTTCAAGACGAGGAAGAGGAGGAGAAAGAGAAAGAAGAGGAAG
ATGTTGGGCAACATTTATTTAACATGCTCCACAGCCCGGACCCCTGGCATCATGCTGCTATTCCTGCAAACTACTGA
AGAAGCATGGGATTTAAATATTTTACTTCTAAATAAATGAATTACTCAATCTCCTATGACCATCTATACATACTC
CACCTTCAAAAAGTACATCAATATTATATCATTAAGGAAATAGTAACCTTCTCTTCTCCAATATGCATGACATTT
TTGGACAATGCAATTGTGGCACTGGCACTTATTTTCAGTGAAGAAAACTTTGTGGTTCTATGGCATTATCATTT
GACAAATGCAAGCATCTTCCTTATCAATCAGCTCCTATTGAACTTACTAGCACTGACTGTGGAATCCTTAAGGGC
CCATTACATTTCTGAAGAAGAAAGCTAAG**ATGA**AGGACATGCCACTCCGAATTCATGTGCTACTTGGCCTAGCTA
TCACTACACTAGTACAAGCTGTAGATAAAAAAGTGGATTGTCCACGGTTATGTACGTGTGAAATCAGGCCTTGGT
TTACACCCAGATCCATTTATATGGAAGCATCTACAGTGGATTGTAATGATTTAGGTCTTTTAACTTTCCAGCCA
GATTGCCAGCTAACACACAGATTCTTCTCCTACAGACTAACAAATATTGCAAAAATTGAATACTCCACAGACTTTC
CAGTAAACCTTACTGGCCTGGATTTATCTCAAAACAATTTATCTTCAGTCACCAATATTAATGTAAAAAAGATGC
CTCAGCTCCTTTCTGTGTACCTAGAGGAAAACAACTTACTGAACTGCCTGAAAAATGTCTGTCCGAACTGAGCA
ACTTACAAGAACTCTATATTAATCACAACTTGCTTTCTACAATTTACCTGGAGCCTTTATTGGCCTACATAATC
TTCTTCGACTTCATCTCAATTCAAATAGATTGCAGATGATCAACAGTAAGTGGTTTGATGCTCTTCCAAATCTAG
AGATTCTGATGATTGGGGAAAATCCAATTATCAGAATCAAAGACATGAACTTTAAGCCTCTTATCAATCTTCGCA
GCCTGGTTATAGCTGGTATAAACCTCACAGAAATACCAGATAACGCCTTGGTTGGACTGGAAAACCTAGAAAGCA
TCTCTTTTTACGATAACAGGCTTATTAAAGTACCCCATGTTGCTCTTCAAAAAGTTGTAAATCTCAAATTTTTGG
ATCTAAATAAAAATCCTATTAATAGAATACGAAGGGGTGATTTTAGCAATATGCTACACTTAAAGAGTTGGGGA
TAAATAATATGCCTGAGCTGATTTCCATCGATAGTCTTGCTGTGGATAACCTGCCAGATTTAAGAAAAATAGAAG
CTACTAACAACCTAGATTGTCTTACATTACCCCAATGCATTTTTCAGACTCCCCAAGCTGGAATCACTCATGC
TGAACAGCAATGCTCTCAGTGCCCTGTACCATGGTACCATTGAGTCTCTGCCAAACCTCAAGGAAATCAGCATAC
ACAGTAACCCCATCAGGTGTGACTGTGTCATCCGTTGGATGAACATGAACAAAACCAACATTGATTTCATGGAGC
CAGATTCACTGTTTTGCGTGGACCCACCTGAATTCOAAGGTGAGAATGTTGCGCAAGTGCATTTTCAGGGACATGA
TGGAAATTTGTCTCCCTCTTATAGCTCCTGAGAGCTTTCCTTCTAATCTAAATGTAGAAGCTGGGAGCTATGTTT
CCTTTCACTGTAGAGCTACTGCAGAACCACAGCCTGAAATCTACTGGATAACACCTTCTGGTCAAAAACCTCTGC
CTAATACCCTGACAGACAAGTTCTATGTCCATTCTGAGGGAACACTAGATATAAATGGCGTAACTCCCAAAGAAG
GGGTTTTATATACTTGTATAGCAACTAACCTAGTTGGCGCTGACTTGAAGTCTGTTATGATCAAAGTGGATGGAT
CTTTTCCACAAGATAACAATGGCTCTTTGAATATTTAAATAAGAGATATTCAGGCCAATTCAGTTTTGGTGTCTT
GGAAAGCAAGTTCTAAAATCTCAAATCTAGTGTTAAATGGACAGCCTTGTCAAGACTGAAAATTCTCATGCTG
CGCAAAGTGCTCGAATACCATCTGATGTCAAGGTATATAATCTTACTCATCTGAATCCATCAACTGAGTATAAAA
TTTGTATTGATATTCACCATCTATCAGAAAAACAGAAAAAATGTGTAAATGTCACCACCAAGGTTTGCACC
CTGATCAAAAAGAGTATGAAAAGAATAATACCACAACACTTATGGCCTGTCTTGGAGGCCTTCTGGGGATTATTG
GTGTGATATGTCTTATCAGCTGCCTCTCTCCAGAAATGAACTGTGATGGTGGACACAGCTATGTGAGGAATTACT
TACAGAAACCAACCTTTGCATTAGGTGAGCTTTATCCTCCTCTGATAAATCTCTGGGAAGCAGGAAAAAGAAAAA
GTACATCACTGAAAGTAAAAGCAACTGTTATAGGTTTACCAACAAATATGTCC**TAAA**AACCAACCAAGGAAACCTA
CTCCAAAAATGAAC

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FIGURE 298

MKDMPLRIHVLLGLAITTLVQAVDKKVDPCRLCTCEIRPWFTPRSIYMEASTVDCNDLGLLTF
PARLPANTQILLQTNNIKIEYSTDFPVNLTGLDLSQNNLSSVTNINVKKMPQLLSVYLEEN
KLTPEKCLSELSNLQELYINHNLLSTISPGAFIGLHNLLRLHLNSNRLQMINSKWFDALPN
LEILMIGENPIIRIKDMNFKPLINLRSLVIAGINLTEIPDNALVGLENLESISFYDNRLIKVP
HVALQKVVNLFKFLDLNKNPINRIRRGDFSNMLHLKELGINNMPELISIDSLAVDNLPDLRKIE
ATNNPRLSYIHPNAFFRLPKLESLMLNSNALSALYHGTIESLPNLKEISIHNPICDCVIRW
MNMNKTNIRFMEPDSLFCVDPPEFQGQNVVRQVHFRDMMEICLPLIAPESFPSNLNVEAGSYVS
FHCRTAEPPQPEIYWITPSGQKLLPNTLTDKFYVHSEGTLDINGVTPKEGGLYTCIATNLVGA
DLKSVMIKVDGSGFPQDNNGSLNIKIRDIQANSVLVSWKASSKILKSSVKWTAFVKTENSAAQ
SARIPSDVKVYNLTHLNPSTEYKICIDIPTIYQKNRKKCVNVTTKGLHPDQKEYEKNNTTTLM
ACLGGLLGIIGVICLISCLSPENNCDDGGHSYVRNYLQKPTFALGELYPPLINLWEAGKEKSTS
LKVKATVIGLPTNMS

Important features:**Signal sequence:**

amino acids 1-22

Transmembrane domain:

amino acids 633-650

N-glycosylation site.amino acids 93-97, 103-107, 223-227, 382-386, 522-526, 579-583,
608-612, 624-628, 625-629**Casein kinase II phosphorylation site.**

amino acids 51-55, 95-99, 242-246, 468-472, 487-491

Tyrosine kinase phosphorylation site.

amino acids 570-579

N-myristoylation site.amino acids 13-19, 96-102, 158-164, 221-227, 352-358, 437-443,
491-497, 492-498, 634-640, 702-708**Cell attachment sequence.**

amino acids 277-280

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FIGURE 299

GCTGTGGGAACCTCTCCACGCGCACGAACTCAGCCAACGATTTCTGATAGATTTTTGGGAGTT
TGACCAGAGATGCAAGGGGTGAAGGAGCGCTTCCTACCGTTAGGGAACTCTGGGGACAGAGCG
CCCCGGCCGCCTGATGGCCGAGGCAGGGTGCGACCCAGGACCCAGGACGGCGTCGGGAACCAT
ACC**ATG**GCCCGGATCCCCAAGACCCTAAAGTTCGTCGTCGTCATCGTCGCGGTCCTGCTGCCA
GTCCTAGCTTACTCTGCCACCACTGCCCCGGCAGGAGGAAGTTCCCCAGCAGACAGTGGCCCCA
CAGCAACAGAGGCACAGCTTCAAGGGGGAGGAGTGTCCAGCAGGATCTCATAGATCAGAACAT
ACTGGAGCCTGTAACCCGTGCACAGAGGGTGTGGATTACACCAACGCTTCCAACAATGAACCT
TCTTGCTTCCCATGTACAGTTTGTAATCAGATCAAAAACATAAAAAGTTCCTGCACCATGACC
AGAGACACAGTGTGTCAGTGTAAAGAAGGCACCTTCCGGAATGAAAACCTCCCCAGAGATGTGC
CGGAAGTGTAGCAGGTGCCCTAGTGGGGAAGTCCAAGTCAGTAATTGTACGTCCTGGGATGAT
ATCCAGTGTGTTGAAGAATTTGGTGCCAATGCCACTGTGGAAACCCAGCTGCTGAAGAGACA
ATGAACACCAGCCCGGGGACTCCTGCCCCAGCTGCTGAAGAGACAATGAACACCAGCCCAGGG
ACTCCTGCCCCAGCTGCTGAAGAGACAATGACCACCAGCCCGGGGACTCCTGCCCCAGCTGCT
GAAGAGACAATGACCACCAGCCCGGGGACTCCTGCCCCAGCTGCTGAAGAGACAATGACCACC
AGCCCGGGGACTCCTGCCTCTTCTCATTACCTCTCATGCACCATCGTAGGGATCATAGTTCTA
ATTGTGCTTCTGATTGTGTTTGTT**TGA**AAGACTTCACTGTGGAAGAAATTCCTTCCTTACCTG
AAAGGTTTCAGGTAGGCGCTGGCTGAGGGCGGGGGGCGCTGGACACTCTCTGCCCTGCCTCCCT
CTGCTGTGTTCCACAGACAGAAACGCCTGC

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FIGURE 300

MARIPKTLKFVVVIVAVLLPVLAYSATTARQEEVPQQTVAPQQQRHSFKGEECPAGSHRSEHT
GACNPCTEGVDYTNASNNEPSCFPCTVCKSDQKHKSSCTMTRDTVCQCKEGTFRNENSPEMCR
KCSRCPSGEVQVSNCTSWDDIQCVEEFGANATVETPAAEETMNTSPGTPAPAAEETMNTSPGT
PAPAAEETMTTSPGTPAPAAEETMTTSPGTPAPAAEETMTTSPGTPASSHYLSCTIVGIIIVLI
VLLLIVFV

Important features:**Signal peptide:**

Amino acids 1-29

Transmembrane domain:

Amino acids 240-259

N-glycosylation site:

Amino acids 77-81;140-144;156-160

cAMP- and cGMP-dependent protein kinase phosphorylation site:

Amino acids 126-130

N-myristoylation sites:

Amino acids 56-62;72-78;114-120;154-160;233-239

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FIGURE 301

CACAAGCATCTTAATTTGAATCCACAAAGTTTCATGTAATGAAAAGAAATACATAATTTTAAT
TCAACCCGAGTGTTTTCCAAGAAGATTGTATTTGCTTAAATTGCTACAGTAATTCAGAGACA
GCCCTGTCTGGACACAGAGTTACTGTGGATTTTTAAGAGACTCAGTTAAAGAATTTAGGAATT
TCTGATTCATTTAAAGGATTTACAAATTCATCAACCCCTGAAACTAAAGCAAATTGAACAGG
AAAAAAAAAAAAAGAAGATGGGTTTTTTAAGTCCAATATATGTTATTTTCTTCTTTTTTGGAGTC
AAAGTACATTGCCAATATGAACTTATCAGTGGGATGAAGACTATGACCAAGAGCCAGATGAT
GATTACCAAACAGGATTTCCCATTTTCGTCAAAATGTAGACTACGGAGTTCCTTTTCATCAGTAT
ACTTTAGGCTGTGTCAGTGAATGCTTCTGTCCAATACTTTCCATCATCAATGTACTGTGAT
AATCGCAAATCAAGACTATCCCAAATATTCGATGCACATTCAGCAACTCTACCTTCAGTTC
AATGAAATTGAGGCTGTGACTGCAAATTCATTCATCAATGCAACTCATCTTAAAGAAATTAAC
CTCAGCCACAACAAAATTAATCTCAAAAGATTGATTATGGTGTGTTTGCTAAGCTTCCAAAT
CTACTACAACCTTCATCTAGAGCATAATAATTTAGAAGAATTTCCATTTCTCTTCTTAAATCT
CTGGAAAGACTCCTTCTTGGTTACAATGAAATCTCCAAACTGCAGACAAATGCTATGGATGGG
CTAGTAAACTTGACCATGCTTGATCTCTGTTATAATTATCTTCATGATTCTCTGCTAAAAGAC
AAAATCTTTGCCAAAATGGAAAACTAATGCAGCTCAACCTCTGCAGTAACAGATTAGAATCA
ATGCCTCCTGGTTTTGCCTTCTTCACTTATGTATCTGTCTTTAGAAAATAATTCAATTTCTTCT
ATACCCGAAAAATACTTCGACAACTTCCAAAACCTTCATACTCTAAGAATGTCACACAACAAA
CTACAAGACATCCCATATAATATTTTTAATCTTCCCAACATTGTAGAACTCAGTGTTGGACAC
AACAAATTGAAGCAAGCATTCTATATTCCAAGAAATTTGGAACACCTATACCTACAAAATAAT
GAAATAGAAAAGATGAATCTTACAGTGATGTGTCCTTCTATTGACCCACTACATTACCACCAT
TTAACATACATTCGTGTGGACCAAATAAACTAAAAGAACCAATAAGCTCATAACATCTTCTTC
TGCTTCCCTCATATACACACTATTTATTATGGTGAACAACGAAGCACTAATGGTCAAACAATA
CAACTAAAGACACAAGTTTTTCAGGAGATTTCCAGATGATGATGATGAAAGTGAAGATCACGAT
GATCCTGACAATGCTCATGAGAGCCCAGAACAAGAAGGAGCAGAAGGGCACTTTGACCTTCAT
TATTATGAAAATCAAGAATAGCAAGAACTATATAGGTATACACTTACGACTTCACAAAACCTA
TACTTAATATAGTAAATCTAAGTAAACATGTATTACTCAAAGTAATATATTTAGAATTATGTA
TTAGTATAAGATCAGAATTGAATTTAAGTTGTTGGTGACATCTGCATCATTTTCATAGGATTAG
AACTTACTCAAATAATGTAAATCTTTAAAAATATAAATTAGAATGACAAGTGGGAATCATAA
ATTAAACGTTAATGGTTTTCTTATGCTCTTTTTTAAATATAGAAATATCATGTTAAAGAAAAAA
AAAAAA

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FIGURE 302

MGFLSPIYVIFFFFGVKVHCQYETYQWDEDDYDQEPDDDDYQTGFPPFRQNVGYGVFPFHQYTLGCV
SECFCPTNFPSSMYCDNRKLKTI PNIPMHIQQLYLQFNEIEAVTANSFINATHLKEINLSHNK
IKSQKIDYGVFAKLPNLLQLHLEHNNLEEFPPPLPKSLERLLLGYNEISKLQTNAMDGLVNLT
MLDLCYNYLHDSLLKDKIFAKMEKLMQLNLCSNRLESMPGPSSLMYLSLENNSSISSIPEKY
FDKLPKLHTLRMSHNKLQDIPYNIFNLPNIVELSVGHNKLKQAFYIPRNLEHLYLQNNIEIEKM
NLTVMCPSIDPLHYHHLTYIRVDQNKLEPISSYIFFCFPHIHTIYYGEQRSTNGQTIQLKTQ
VFRFPDDDDDESEDHDDPDNAHESPEQEGAEGHFDLHYENQE

Important features:**N-glycosylation sites:**

Amino acids 113-117;121-125; 187-191;242-246;316-320

Tyrosine kinase phosphorylation sites:

Amino acids 268-275;300-307

N-myristoylation site:

Amino acids 230-236

Leucine zipper patterns:

Amino acids 146-168;217-239

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FIGURE 303

GCCCGGGACTGGCGCAAGGTGCCCAAGCAAGGAAAGAAATAATGAAGAGACACATGTGTTAGC
TGCAGCCTTTTGAACACGCAAGAAGGAAATCAATAGTGTGGACAGGGCTGGAACCTTTACCA
CGCTTGTTGGAGTAGATGAGGAATGGGCTCGTGATTATGCTGACATTCCAGCATGAATCTGGT
AGACCTGTGGTTAACCCGTTCCCTCTCCATGTGTCTCCTCCTACAAAGTTTTGTTCTTATGAT
ACTGTGCTTTTCATTCTGCCAGTATGTGTCCCAAGGGCTGTCTTTGTTCTTCCTCTGGGGGTTT
AAATGTCACCTGTAGCAATGCAATCTCAAGGAAATACCTAGAGATCTTCCTCCTGAAACAGT
CTTACTGTATCTGGACTCCAATCAGATCACATCTATTCCCAATGAAATTTTAAAGGACCTCCA
TCAACTGAGAGTTCTCAACCTGTCCAAAATGGCATTGAGTTTATCGATGAGCATGCCTTCAA
AGGAGTAGCTGAAACCTTGCGACTCTGGACTTGTCCGACAATCGGATTCAAAGTGTGCACAA
AAATGCCTTCAATAACCTGAAGGCCAGGGCCAGAATTGCCAACAACCCCTGGCACTGCGACTG
TACTCTACAGCAAGTTCTGAGGAGCATGGCGTCCAATCATGAGACAGCCCACAACGTGATCTG
TAAAACGTCCGTGTTGGATGAACATGCTGGCAGACCATTCTCAATGCTGCCAACGACGCTGA
CCTTTGTAACCTCCCTAAAAAACTACCGATTATGCCATGCTGGTCACCATGTTTGGCTGGTT
CACTATGGTGATCTCATATGTGGTATATTATGTGAGGCAAAATCAGGAGGATGCCCGGAGACA
CCTCGAATACTTGAAATCCCTGCCAAGCAGGCAGAAGAAAGCAGATGAACCTGATGATATTAG
CACTGTGGTATTAGTGTCCAACTGACTGTCATTGAGAAAGAAAGAAAGTAGTTTGCGATTGCA
GTAGAAATAAGTGGTTTACTTCTCCCATCCATTGTAAACATTTGAACTTTGTATTTTCAGTTT
TTTTTGAATTATGCCACTGCTGAACTTTTAAACAAACACTACAACATAAATAATTTGAGTTTAG
GTGATCCACCCCTTAATTGTACCCCGATGGTATATTTCTGAGTAAGCTACTATCTGAACATT
AGTTAGATCCATCTCACTATTTAATAATGAAATTTATTTTTTTAATTTAAAAGCAAATAAAAG
CTTAACCTTGAACCATGGGAAAAAAAAAAAAAAAAAAAAAACA

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FIGURE 304

MNLVDLWLTRSLSMCLLLQSFVLMILCFHSASMCPKGCLCSSSGGLNVTC SNANLKEIPRDLP
PETVLLYLDSNQITSIPNEIFKDLHQLRVLNLSKNGIEFIDEHAFKGVAETLQTLDSLSDNRIQ
SVHKNAFNNLKARARIANNPWHCDCTLQQVLRSMASNHETAHNVICKTSVLDEHAGRPFLNAA
NDADLCNLPKKT TDYAMLVTMFGWFTMVISYVVYYVRQNQEDARRHLEYLKSLPSRQKKADEP
DDISTVV

Important features:**Signal sequence:**

Amino acids 1-33

Transmembrane domain:

Amino acids 204-219

N-glycosylation sites:

Amino acids 47-51;94-98

cAMP- and cGMP-dependent protein kinase phosphorylation site:

Amino acids 199-203

Casein kinase II phosphorylation site.

amino acids 162-166, 175-179

N-myristoylation sites:

Amino acids 37-43;45-51;110-116

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FIGURE 305

CGCCACCACTGCGGCCACCGCCA**ATG**AAACGCCTCCCGCTCCTAGTGGTTTTTTCCACTTTGTTGAATTGTTCCCT
ATACTCAAAATGACCAAGACACCTTGTCTCCCAAATGCAAAATGTGAAATACGCAATGGAATTGAAGCCTGCT
ATTGCAACATGGGATTTTTCAGGAAATGGTGTCAACAATTTGTGAAGATGATAATGAATGTGGAAATTTAACTCAGT
CCTGTGGCGAAAAATGCTAATTGCACTAACACAGAAGGAAGTTATTATTGTATGTGTGTACCTGGCTTCAGATCCA
GCAGTAACCAAGACAGGTTTATCACTAATGATGGAACCGTCTGTATAGAAAATGTGAATGCAAACCTGCCATTTAG
ATAATGTCTGTATAGCTGCAAAATATTAATAAAACTTTAACAATAATCAGATCCATAAAAGAACCTGTGGCTTTGC
TACAAGAAGTCTATAGAAATCTGTGACAGATCTTTCACCAACAGATATAATTACATATATAGAAATATTAGCTG
AATCATCTTCATTACTAGGTTACAAGAACAACACTATCTCAGCCAAGGACACCCTTTCTAACTCAACTCTTACTG
AATTTGTAAAAACCGTGAATAATTTTGTTCAAAGGGATACATTTGTAGTTTGGGACAAGTTATCTGTGAATCATA
GGAGAACACATCTTACAAAACCTCATGCACACTGTTGAACAAGCTACTTTAAGGATATCCAGAGCTTCCAAAAGA
CCACAGAGTTTGATACAAATTCACGGATATAGCTCTCAAAGTTTTCTTTTTTGATTTCATATAACATGAAACATA
TTCATCCTCATATGAATATGGATGGAGACTACATAAATATATTTCCAAAGAGAAAAGCTGCATATGATTCAAATG
GCAATGTTGCAGTTGCATTTTTATATTATAAGAGTATTGGTCCCTTTGCTTTCATCATCTGACAACCTCTTATTGA
AACCTCAAAATATGATAATTCTGAAGAGGAGGAAAGAGTCATATCTTCAGTAATTTTCAGTCTCAATGAGCTCAG
ACCCACCCACATTATATGAACCTTGAAAAATAACATTTACATTAAGTCATCGAAAGGTCACAGATAGGTATAGGA
GTCTATGTGCATTTTGGAAATTACTCACCTGATACCATGAATGGCAGCTGGTCTTCAGAGGGCTGTGAGCTGACAT
ACTCAAATGAGACCCACACCTCATGCCGCTGTAATCACCTGACACATTTTGCAATTTTGATGTCTCTGGTCCCTT
CCATTGGTATTAAAGATTATAATATTCTTACAAGGATCACTCAACTAGGAATAATTATTTCACTGATTTGTCTTG
CCATATGCATTTTTACCTTCTGGTTCTTCAGTGAAATTCAAAGCACCAGGACAACAATTCACAAAAATCTTTGCT
GTAGCCTATTTCTTGCTGAACCTGTTTTCTTGTGGGATCAATACAAATACTAATAAGCTCTTCTGTTCAATCA
TTGCCGGACTGCTACACTACTTCTTTTTTAGCTGCTTTTGCATGGATGTGCATTGAAGGCATACATCTCTATCTCA
TTGTTGTGGGTGTCATCTACAACAAGGGATTTTTTGACAAGAATTTTTATATCTTTGGCTATCTAAGCCCAGCCG
TGGTAGTTGGATTTTCGGCAGCACTAGGATACAGATATTATGGCACAACCAAAGTATGTTGGCTTAGCACCGAAA
ACAACCTTTATTTGGAGTTTTATAGGACCAGCATGCCTAATCATCTTGTTAATCTCTTGGCTTTTGGAGTCATCA
TATACAAAGTTTTTCGTCCACTGCAGGGTTGAAACCAGAAGTTAGTTGCTTTGAGAACATAAGGTCTTGTGCAA
GAGGAGCCCTCGCTCTTCTGTTCCCTCTCGGCACCACCTGGATCTTTGGGGTTCTCCATGTTGTGCACGCATCAG
TGGTTACAGCTTACCTCTTCACAGTCAGCAATGCTTTCCAGGGGATGTTCAATTTTTTTTATTCTGTGTGTTTTAT
CTAGAAAGATTCAAGAAGAATATTACAGATTGTTCAAAAATGTCCCCTGTTGTTTTGGATGTTTAAGG**TAA**ACAT
AGAGAATGGTGGATAATTACAACCTGCACAAAAATAAAAATTCGAAGCTGTGGATGACCAATGTATAAAAATGACT
CATCAAATTATCCAATTATTAACCTACTAGACAAAAAGTATTTTAAATCAGTTTTTCTGTTTATGCTATAGGAACT
GTAGATAATAAGGTAAAATTATGTATCATATAGATATACTATGTTTTTCTATGTGAAATAGTTCTGTCAAAAATA
GTATTGCAGATATTGGAAGTAATTGTTTTCTCAGGAGTGATATCACTGCACCCAAGGAAAGATTTTCTTTCTA
ACACGAGAAGTATATGAATGTCCTGAAGGAAACCACTGGCTTGATATTTCTGTGACTCGTGTTGCCTTTGAAACT
AGTCCCCTACCACCTCGGTAATGAGCTCCATTACAGAAAGTGGAACATAAGAGAATGAAGGGGCAGAATATCAAA
CAGTGAAAAGGGAATGATAAGATGTATTTTGAATGAACTGTTTTTCTGTAGACTAGCTGAGAAATTGTTGACAT
AAAATAAAGAATTGAAGAAACACATTTTACCATTTTGTGAATTGTTCTGAACTTAAATGTCCACTAAAAACAACCT
AGACTTCTGTTTGCTAAATCTGTTTCTTTTTCTAATATTCTAAAAAAGGTTTACCTCCACAAATTGA
AA

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FIGURE 306

MKRLPLLVVFSTLLNCSYTQÑCTKTPCLPNAKCEIRNGIEACYCNMGFSGNGVTICEDDNECGNLTQSCGENANC
TNTGSSYYCMCVPGFRSSSNQDRFITNDGTVCIENTVNANCHLDNVCIAANINKTLTKIRSIKEPVALLQEVYRNS
VTDLSPTDIITYIEILAESSSLLGYKNNTISAKDTLSNSTLTEFVKTVNNFVQRDTFVVWDKLSVNHRRTHLTKL
MHTVEQATLRISQSFQKTTEFDTNSTDIALKVFFFDSDYNMKHIHPHMNMDGDYINIFPKRKAAYDSNGNVAVAFL
YYKSIGPLLSSSDNFLKQPQNYDNSEEEERVISSVISVSMSSNPPTLYELEKITFTLSHRKVTDYRSLCAFWNY
SPDTMNGSWSSEGCETYSNETHTSCRCNHLTHFAILMSSGPSIGIKDYNILTRITQLGIIISLICLAICIFTFW
FFSEIQSTRTTIHKNLCCSLFLAELVFLVGINTNTNKLFCSEIAGLLHYFFLAFAWMCIEGIHLYLIVVGVIYN
KGFLHKNFYIFGYLSPAVVVGFSAAALGYRYYGTTKVCWLSTENNFWSFIGPACLIILVNLLAFGVIIYKVRHT
AGLKPEVSCFENIRSCARGALALLFLLGTTWIFGVLHVHASVVTAYLFTVSNAFQGMFIFLFLCVLSRKIQEEY
YRLFKNVPCCFGCLR

Important features:**Signal peptide:**

Amino acids 1-19

Transmembrane domain:

Amino acids 431-450;494-515;573-594;619-636;646-664

N-glycosylation sites:Amino acids 15-19;21-25;64-68;74-78;127-131;177-181;
188-192;249-253;381-385;395-399**Glycosaminoglycan attachment site:**

Amino acids 49-53

cAMP- and cGMP-dependent protein kinase phosphorylation site:

Amino acids 360-364

Tyrosine kinase phosphorylation sites:

Amino acids 36-44;670-677

N-myristoylation sites:Amino acids 38-44;50-56;52-58;80-86;382-388;388-394;
434-440;480-486;521-527**Aspartic acid and asparagine hydroxylation site:**

Amino acids 75-87

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FIGURE 307

CCAGGCCGGGAGGCGACGCGCCAGCCGTCTAAACGGGAACAGCCCTGGCTGAGGGAGCTGCAGCGCAGCAGAGT
ATCTGACGGCGCCAGGTTGCGTAGGTGCGGCACGAGGAGTTTTCCCGGCAGCGAGGAGGTCCTGAGCAGCATGGC
CCGGAGGAGCGCCTTCCCTGCCGCGCTCTGGCTCTGGAGCATCCTCCTGTGCCTGCTGGCACTGCGGGCGGA
GGCCGGGCGCCGCGCAGGAGGAGAGCCTGTACCTATGGATCGATGCTCACCAGGCAAGAGTACTCATAGGATTTGA
AGAAGATATCCTGATTGTTTCAGAGGGGAAAATGGCACCTTTTACACATGATTTTCAGAAAAGCGCAACAGAGAAT
GCCAGCTATTCTGTCAATATCCATTCATGAATTTTACCTGGCAAGCTGCAGGGCAGGCAGAATACTTCTATGA
ATTCCTGTCTTGCGCTCCCTGGATAAAGGCATCATGGCAGATCCAACCGTCAATGTCCCTCTGCTGGGAACAGT
GCCTCACAAGGCATCAGTTGTTCAAGTTGGTTTCCCATGTCTTGGAACAGGATGGGGTGGCAGCATTTGAAGT
GGATGTGATTGTTATGAATTCCTGAAGGCAACACCATTCTCCAAACACCTCAAATGCTATCTTCTTTAAACATG
TCAACAAGCTGAGTGCCAGGCGGGTGCCGAAATGGAGGCTTTTGTAAATGAAAGACGCATCTGCGAGTGTCTTGA
TGGGTTCCACGGACCTCACTGTGAGAAAGCCCTTTGTACCCACGATGTATGAATGGTGGACTTTGTGTGACTCC
TGGTTTCTGCATCTGCCCACCTGGATTCTATGGAGTGAAGTGTGACAAAGCAAAGTCTCAACCACCTGCTTTAA
TGGAGGGACCTGTTTCTACCCCTGGAAAATGTATTTGCCCTCCAGGACTAGAGGGAGAGCAGTGTGAAATCAGCAA
ATGCCCACAACCTGTGAAATGGAGGTAAATGCATTGGTAAAAGCAAATGTAAGTGTTCCAAAGGTTACCAGGG
AGACCTCTGTTCAAAGCCTGTCTGCGAGCCTGGCTGTGGTGCACATGGAACCTGCCATGAACCCAACAAATGCCA
ATGTCAAGAAGGTTGGCATGGAAGACACTGCAATAAAAGGTACGAAGCCAGCCTCATACATGCCCTGAGGCCAGC
AGGCGCCAGCTCAGGCAGCACACGCCTTCACTTAAAAAGGCCGAGGAGCGGCGGGATCCACCTGAATCCAATTA
CATCTGGTGAACTCCGACATCTGAAACGTTTTTAAGTTACACCAAGTTCATAGCCTTTGTTAACCTTTTCATGTGT
GAATGTTCAAATAATGTTTATTACCTTAAGAATACTGGCCTGAATTTTATTAGCTTCATTATAAATCACTGAGC
TGATATTTACTCTTCCTTTTAAGTTTTCTAAGTACGTCTGTAGCATGATGGTATAGATTTTCTTGTTTCAGTGCT
TTGGGACAGATTTTATATTATGTCAATTGATCAGGTTAAAATTTTCAGTGTGTAGTTGGCAGATATTTTCAAAT
TACAATGCATTTATGGTGTCTGGGGGAGGGGAACATCAGAAAGGTTAAATTGGGCAAAATGCGTAAGTCACAA
GAATTTGGATGGTGCAGTTAATGTTGAAGTTACAGCATTTTCAGATTTTATTGTGAGATATTTAGATGTTTGTAC
ATTTTTAAAAATTGCTCTTAATTTTTAACTCTCAATACAATATATTTTGACCTTACCATTATTCCAGAGATTCA
GTATTAATAAAAAAAAAAATTACACTGTGGTAGTGGCATTATAACAATATAATATATTCTAAACACAATGAAATAG
GGAATATAATGTATGAACCTTTTGCATTGGCTTGAAGCAATATAATATATTGTAACAAAACACAGCTCTTACCT
AATAAACATTTTATACTGTTTGTATGTATAAAATAAAGGTGCTGCTTTAGTTTTTTGGAAAAAAAAAAAAAAAAA
AAAAAAA

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FIGURE 308

MARRSAFPAAALWLWSILLCLLALRAEAGPPQEESLYLWIDAHQARVLIGFEEDILIVSEGKM
APFTHDFRKAQQRMPAIPVNIHSMNFTWQAAGQAEYFYEFLLSLRSLDKGIMADPTVNVPLLGT
VPHKASVVQVGFPCLGKQDGVAAFEVDVIVMNSEGNTILQTPQNAIFFKTCQQAECPPGGCRNG
GFCNERRICECPDGFHGPHEKALCTPRCMNGGLCVTPGFCICPPGFYGVNCDKANCSTTCFN
GGTCFYPGKCICPPGLEGEQCEISKCPQPCRNGGKCKGSKCKCSKGYQGDLCSPVCEPGCG
AHGTCHEPNKCQCQEGWHGRHCNKRYEASLIHALRPAGAQLRQHTPSLKKAEEERRDPPESNYIW

Important features:**Signal sequence:**

Amino acids 1-28

N-glycosylation sites:

Amino acids 88-92;245-249

Tyrosine kinase phosphorylation site:

Amino acids 370-378

N-myristoylation sites:

Amino acids 184-190;185-191;189-195;315-321

ATP/GTP-binding site motif A (P-loop):

Amino acids 285-293

EGF-like domain cysteine pattern signatures:

Amino acids 198-210;230-242;262-274;294-306;326-338

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FIGURE 309

CCCACGCGTCCGGTCTCGCTCGCTCGCGCAGCGGCGGCAGCAGAGGTCGCGCACAGATGCGGG
TTAGACTGGCGGGGGGAGGAGGCGGAGGAGGGAAGGAAGCTGCATGCATGAGACCCACAGACT
CTTGCAAGCTGGATGCCCTCTGTGGATGAAAG**ATG**TATCATGGAATGAACCCGAGCAATGGAG
ATGGATTTCTAGAGCAGCAGCAGCAGCAGCAACCTCAGTCCCCCAGAGACTCTTGGCCG
TGATCCTGTGGTTTCAGCTGGCGCTGTGCTTCGGCCCTGCACAGCTCACGGGCGGGTTCGATG
ACCTTCAAGTGTGTGCTGACCCCGGCATTCCCGAGAATGGCTTCAGGACCCCGAGCGGAGGGG
TTTTCTTTGAAGGCTCTGTAGCCCGATTTCACTGCCAAGACGGATTCAAGCTGAAGGGCGCTA
CAAAGAGACTGTGTTTGAAGCATTTTAAATGGAACCCTAGGCTGGATCCCAAGTGATAATTCCA
TCTGTGTGCAAGAAGATTGCCGTATCCCTCAAATCGAAGATGCTGAGATTCATAACAAGACAT
ATAGACATGGAGAGAAGCTAATCATCACTTGTTCATGAAGGATTCAAGATCCGGTACCCCGACC
TACACAATATGGTTTCATTATGTCGCGATGATGGAACGTGGAATAATCTGCCCATCTGTCAAG
GCTGCCTGAGACCTCTAGCCTCTTCTAATGGCTATGTAAACATCTCTGAGCTCCAGACCTCCT
TCCCGGTGGGGACTGTGATCTCCTATCGCTGCTTTCCCGGATTTAAACTTGATGGGTCTGCGT
ATCTTGAGTGCTTACAAAACCTTATCTGGTCGTCCAGCCCACCCCGGTGCCTTGCTCTGGAAG
CCCAAGTCTGTCCACTACCTCCAATGGTGAGTCACGGAGATTTTCGTCTGCCACCCGCGGCCTT
GTGAGCGCTACAACCACGGAACCTGTGGTGAGTTTTACTGCGATCCTGGCTACAGCCTCACCA
GCGACTACAAGTACATCACCTGCCAGTATGGAGAGTGGTTTCCTTCTTATCAAGTCTACTGCA
TCAAATCAGAGCAAACGTGGCCCAGCACCCATGAGACCCTCCTGACCACGTGGAAGATTGTGG
CGTTCACGGCAACCAGTGTGCTGCTGGTGCTGCTGCTCGTCATCCTGGCCAGGATGTTCCAGA
CCAAGTTCAAGGCCCACTTTCCCCCAGGGGGCCTCCCCGGAGTTCCAGCAGTGACCCTGACT
TTGTGGTGGTAGACGGCGTGCCCGTCATGCTCCCGTCCTATGACGAAGCTGTGAGTGGCGGCT
TGAGTGCCTTAGGCCCCGGGTACATGGCCTCTGTGGGGCCAGGGCTGCCCCTTACCCGTGGACG
ACCAGAGCCCCCAGCATACCCCGGCTCAGGGGACACGGACACAGGCCCAGGGGAGTCAGAAA
CCTGTGACAGCGTCTCAGGCTCTTCTGAGCTGCTCCAAAGTCTGTATTACCTCCCAGGTGCC
AAGAGAGCACCCACCCTGCTTCGGACAACCCTGACATAATTGCCAGCACGGCAGAGGAGGTGG
CATCCACCAGCCCAGGCATCCATCATGCCCACTGGGTGTTGTTCCCTAAGAACT**TGA**ATTGATTA
AAAAATTTCCCAAAGTGTCTGAAGTGTCTCTTCAAATACATGTTGATCTGTGGAGTTGATTC
CTTTCCTTCTCTTGGTTTTAGACAAATGTAAACAAAGCTCTGATCCTTAAAATTGCTATGCTG
ATAGAGTGGTGAGGGCTGGAAGCTTGATCAAGTCCTGTTTCTTCTTGACACAGACTGATTAAA
AATTAAAAGNAAAAAA

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FIGURE 310

MYHGMNPSNGDGFLEQQQQQQPQSPQRL LAVILWFQLALCFGPAQLTG GFDDLQVCADPGIP
ENGFRTPSGGVFFEGSVARFHCQDGFKLKGATKRLCLKHFNGTLGWIPSDNSICVQEDCRIPQ
IEDAEIHNKTYRHGEKLIITCHEGFKIRYPDLHNMVSLCRDDGTWNNLPICQGCLRPLASSNG
YVNISELQTSFPVGTVISYRCFPGFKLDGSAYLECLQNLIWSSSPRCLALEAQVCPLPPMVS
HGDFVCHPRPCERYNHGTVVEFYCDPGYSLTSDYKYITCQYGEWFPSYQVYCIKSEQTWPSTH
ETLLTTWKIVAFTATSVLLVLLLVILARMFQTKFKAHFPPRGPPRSSSSDPDFVVVDGVPVML
PSYDEAVSGGLSALGPGYMASVGQGCPLPVDDQSPPAYPGSGDTDTGPGESETCDSVSGSSEL
LQSLYSPPRCQESTHPASDNPDI IASTAEVASTSPGIHHAHWLFLRN

Important features:**Signal sequence:**

amino acids 1-41

Transmembrane domain:

amino acids 325-344

N-glycosylation site.

amino acids 104-108, 134-138, 192-196

Casein kinase II phosphorylation site.amino acids 8-12, 146-150, 252-256, 270-274, 313-317, 362-366,
364-368, 380-384, 467-471, 468-472**N-myristoylation site.**amino acids 4-10, 61-67, 169-175, 203-209, 387-393, 418-424,
478-484**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 394-405

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FIGURE 311

CAGCGCGTGGCCGGCGCCGCTGTGGGGACAGCATGAGCGGCGGTTGGATGGCGCAGGTTGGAG
CGTGGCGAACAGGGGCTCTGGGCCTGGCGCTGCTGCTGCTGCTCGGCCTCGGACTAGGCCTGG
AGGCCGCCGCGAGCCCGCTTTCCACCCCGACCTCTGCCCAGGCCGCAGGCCCCAGCTCAGGCT
CGTGCCCAACCCACCAAGTTCCAGTGCCGCACCAGTGGCTTATGCGTGCCCTCACCTGGCGCT
GCGACAGGGACTTGGACTGCAGCGATGGCAGCGATGAGGAGGAGTGCAGGATTGAGCCATGTA
CCCAGAAAGGGCAATGCCACCGCCCCCTGGCCTCCCCTGCCCTGCACCGGCGTCAGTGACT
GCTCTGGGGGAAGTGCACAAGAACTGCGCAACTGCAGCCGCCTGGCCTGCCTAGCAGGCGAGC
TCCGTTGCACGCTGAGCGATGACTGCATTCCACTCACGTGGCGCTGCGACGGCCACCCAGACT
GTCCCGACTCCAGCGACGAGCTCGGCTGTGGAACCAATGAGATCCTCCCGGAAGGGGATGCCA
CAACCATGGGGCCCCCTGTGACCCTGGAGAGTGTACCTCTCTCAGGAATGCCACAACCATGG
GGCCCCCTGTGACCCTGGAGAGTGTCCCCTCTGTGCGGAATGCCACATCCTCCTCTGCCGGAG
ACCAGTCTGGAAGCCCAACTGCCTATGGGGTTATTGCAGCTGCTGCGGTGCTCAGTGCAAGCC
TGGTCACCGCCACCCTCCTCCTTTTGTCTGGCTCCGAGCCCAGGAGCGCCTCCGCCCCACTGG
GGTTACTGGTGGCCATGAAGGAGTCCCTGCTGCTGTCAGAACAGAAGACCTCGCTGCCCTTGAG
GACAAGCACTTGCCACCACCGTCACTCAGCCCTGGGCGTAGCCGGACAGGAGGAGAGCAGTGA
TGCGGATGGGTACCCGGGCACACCAGCCCTCAGAGACCTGAGTTCTTCTGGCCACGTGGAACC
TCGAACCCGAGCTCCTGCAGAAGTGGCCCTGGAGATTGAGGGTCCCTGGACACTCCCTATGGA
GATCCGGGGAGCTAGGATGGGGAACCTGCCACAGCCAGAACTGAGGGGCTGGCCCCAGGCAGC
TCCCAGGGGGTAGAACGGCCCTGTGCTTAAGACACTCCCTGCTGCCCCGTCTGAGGGTGGCGA
TTAAAGTTGCTTC

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FIGURE 312

MSGGWMAQVGAWRTGALGLALLLLLGLGLGLEAAASPLSTPTSAQAAGPSSGSCPPTKFQCRT
SGLCVPLTWRCRDLDCSDGSDEEECRIEPCCTQKGQCPPPPGLPCPCTGVSDCSGGTDKKLRN
CSRLACLAGELRCTLSDDCIPLTWRCDGHPDCPDSSDELGCGTNEILPEGDATTMGPPVTLES
VTSLRNATTMGPPVTLESVPSVGNATSSSAGDQSGSPTAYGVIAAAVLSASLVTATLLLLSW
LRAQERLRPLGLLVAMKESLLLSEQKTSLP

Important features:**Signal sequence:**

Amino acids 1-30

Transmembrane domain:

Amino acids 231-248

N-glycosylation sites:

Amino acids 126-130;195-199;213-217

Casein kinase II phosphorylation site.

amino acids 84-88, 140-144, 161-165, 218-222

N-myristoylation sites:Amino acids 3-9;10-16;26-32;30-36;112-118;166-172;212-218;
224-230;230-236;263-269**Prokaryotic membrane lipoprotein lipid attachment site:**

Amino acids 44-55

Leucine zipper pattern:

Amino acids 17-39

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FIGURE 313

CGGACGCGTGGGCGTCCGGCGGTTCGACAGCCAGGAGGCGGAGGCGCGGGCCAGCCTGGGCCCCAGCCCACAC
CTTCACCAGGGCCCAGGAGCCACCATGTTGGCGATGTCCACTGGGGCTACTGCTGTTGCTGCCGCTGGCTGGCCAC
TTGGCTCTGGGTGCCCAGCAGGGTCGTGGGCGCCGGGAGCTAGCACCGGGTCTGCACCTGCCGGGCATCCGGGAC
GCGGGAGGCCGGTACTGCCAGGAGCAGGACCTGTGCTGCCGCGGCCGTGCCGACGACTGTGCCCTGCCCTACCTG
GGCGCCATCTGTTACTGTGACCTCTTCTGCAACCGCACGGTCTCCGACTGCTGCCCTGACTTCTGGGACTTCTGC
CTCGGCGTGCCACCCCCTTTTCCCCCGATCCAAGGATGTATGCATGGAGGTCGTATCTATCCAGTCTTGGGAACG
TACTGGGACAACCTGTAACCGTTGCACCTGCCAGGAGAACAGGCAGTGGCATGGTGGATCCAGACATGATCAAAGC
CATCAACCAGGGCAACTATGGCTGGCAGGCTGGGAACCACAGCGCCTTCTGGGGCATGACCCTGGATTGAGGGCAT
TCGCTACCGCCTGGGCACCATCCGCCCATCTTCTCGGTGCATGAACATGCATGAAATTTATACAGTGCTGAACCC
AGGGGAGGTGCTTCCCACAGCCTTCGAGGCCTCTGAGAAGTGGCCCAACCTGATTCATGAGCCTCTTGACCAAGG
CAACTGTGCAGGCTCCTGGGCCTTCTCCACAGCAGCTGTGGCATCCGATCGTGTCTCAATCCATTCTCTGGGACA
CATGACGCCTGTCCTGTCGCCCCAGAACCTGCTGTCTTGTGACACCCACCAGCAGCAGGGCTGCCGCGGTGGGCG
TCTCGATGGTGCTGGTGGTTCCCTGCGTCGCGCGAGGGGTGGTGTCTGACCACTGCTACCCCTTCTCGGGCCGTGA
ACGAGACGAGGCTGGCCCTGCGCCCCCTGTATGATGCACAGCCGAGCCATGGGTCCGGGCAAGCGCCAGGCCAC
TGCCCACTGCCCCAACAGCTATGTTAATAACAATGACATCTACCAGGTCACTCCTGTCTACCGCCTCGGCTCCAA
CGACAAGGAGATCATGAAGGAGCTGATGGAGAATGGCCCTGTCCAAGCCCTCATGGAGGTGCATGAGGACTTCTT
CCTATACAAGGGAGGCATCTACAGCCACACGCCAGTGAGCCTTGGGAGGCCAGAGAGATACCGCCGGCATGGGAC
CCACTCAGTCAAGATCACAGGATGGGGAGAGGAGACGCTGCCAGATGGAAGGACGCTCAAATACTGGACTGCGGC
CAACTCCTGGGGCCCAGCCTGGGGCGAGAGGGGCCACTTCCGCATCGTGCGCGGCGTCAATGAGTGCGACATCGA
GAGCTTCGTGCTGGGCGTCTGGGGCCGCGTGGGCATGGAGGACATGGGTCACTGAGGCTGCGGGCACACGC
GGGGTCCGGCCTGGGATCCAGGCTAAGGGCCGGCGGAAGAGGGCCCCAATGGGGCGGTGACCCCAGCCTCGCCGA
CAGAGCCCCGGGGCGCAGGCGGGCGCCAGGGCGCTAATCCCGCGCGGGTTCGCTGACGCAGCGCCCCGCCTGGG
AGCCGCGGGCAGGCGAGACTGGCGGAGCCCCCAGACCTCCAGTGGGGACGGGGCAGGGCCTGGCCTGGGAAGAG
CACAGCTGCAGATCCCAGGCCTCTGGCGCCCCCACTCAAGACTACCAAAGCCAGGACACCTCAAGTCTCCAGCCC
CAATACCCCAACCCCAATCCCGTATTCTTTTTTTTTTTTTTTTAGACAGGGTCTTGCTCCGTTGCCAGGTTGGAG
TGCAGTGGCCCATCAGGGCTCACTGTAACCTCCGACTCCTGGGTTCAGTGACCCTCCCACCTCAGCCTCTCAAG
TAGCTGGGACTACAGGTGCACCACCACACCTGGCTAATTTTTGTATTTTTGTAAAGAGGGGGGTCTCACTGTGT
TGCCCAGGCTGGTTTCGAACTCCTGGGCTCAAGCGGTCCACCTGCCTCCGCCTCCCAAAGTGCTGGGATTGCAGG
CATGAGCCACTGCACCCAGCCCTGTATTCTTATTCTTCAGATATTTATTTTTCTTTTCACTGTTTTAAATAAAAA
CCAAAGTATTGATAAAAAAAAAA

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FIGURE 314

MWRCPLGLLLLLPLAGHLALGAQQGRGRRELAPGLHLRGIRDAGGRYCQEQLCCRGRADDCA
LPYLGAICYCDLFCNRTVSDCCPDFWDFCLGVPPFPPIQGCMHGGRIYPVLGTYWDNCNRCT
CQENRQWHGGSRHDQSHQPGQLWLAGWEPQRLLGHDPG

Important features:**N-glycosylation site.**

amino acids 78-82, 161-165

Casein kinase II phosphorylation site.

amino acids 80-84, 117-121, 126-130, 169-173, 205-209, 296-300,
411-415

N-myristoylation site.

amino acids 21-27, 39-45, 44-50, 104-110, 160-164, 224-230,
269-275, 378-384, 442-448

Amidation site.

amino acids 26-30, 318-322

Eukaryotic thiol (cysteine) proteases histidine active site.

amino acids 398-409

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FIGURE 315

CGGACGCGTGGGCCCCTGGTGGGCCCAGCAAGATGGATCTACTGTGGATCCTGCCCTCCCTGT
GGCTTCTCCTGCTTGGGGGGCCTGCCTGCCTGAAGACCCAGGAACACCCCAGCTGCCCAGGAC
CCAGGGAACTGGAAGCCAGCAAAGTTGTCCTCCTGCCCAGTTGTCCCGGAGCTCCAGGAAGTC
CTGGGGAGAAGGGAGCCCCAGGTCCTCAAGGGCCACCTGGACCACCAGGCAAGATGGGCCCCA
AGGGTGAGCCAGGCCCCAGAACTGCCGGGAGCTGTTGAGCCAGGGCGCCACCTTGAGCGGCT
GGTACCATCTGTGCCTACCTGAGGGCAGGGCCCTCCCAGTCTTTTGTGACATGGACACCGAGG
GGGGCGGCTGGCTGGTGTTCAGAGGGCGCCAGGATGGTTCTGTGGATTTCTTCCGCTCTTGGT
CCTCCTACAGAGCAGGTTTTGGGAACCAAGAGTCTGAATTCTGGCTGGGAAATGAGAATTTGC
ACCAGCTTACTCTCCAGGGTAACTGGGAGCTGCGGGTAGAGCTGGAAGACTTTAATGGTAACC
GTACTTTCGCCCCTATGCGACCTTCCGCCTCCTCGGTGAGGTAGACCACTACCAGCTGGCAC
TGGGCAAGTTCTCAGAGGGCACTGCAGGGGATTCCCTGAGCCTCCACAGTGGGAGGCCCTTTA
CCACCTATGACGCTGACCACGATTCAAGCAACAGCAACTGTGCAGTGATTGTCCACGGTGCCT
GGTGGTATGCATCCTGTTACCGATCAAATCTCAATGGTCGCTATGCAGTGTCTGAGGCTGCCG
CCCACAAATATGGCATTGACTGGGCCTCAGGCCGTGGTGTGGGCCACCCCTACCGCAGGGTTC
GGATGATGCTTCGATTAGGGGCACTCTGGCAGCCAGTGCCCTTATCTCTCCTGTACAGCTTCCGG
ATCGTCAGCCACCTTGCCTTTGCCAACCACCTCTGCTTGCCTGTCCACATTTAAAAATAAAAT
CATTTTAGCCCTTTCA

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FIGURE 316

MDLLWILPSLWLLLLGGPACLKTQEHPSCPGPRELEASKVVLLPSCPGAPGSPGEKGAPGPQG
PPGPPGKMGPKGEPGPRNCRELLSQGATLSGWYHLCLPEGRALPVFCDMDTEGGGWLVFQRRQ
DGSVDFFRSWSSYRAGFGNQESEFWLGNENLHQLTLQGNWELRVELEDFNGNRTFAHYATFRL
LGEVDHYQLALGKFSEGTAGDSLHSGRPFTTYDADHDSSNSNCAVIVHGAWWYASCYRSNL
NGRYAVSEAAAHKYGIDWASGRGVGHPYRRVRMMLR

Important features:**Signal peptide:**

Amino acids 1-16

N-glycosylation site:

Amino acids 178-182

Glycosaminoglycan attachment site:

Amino acids 272-276

Tyrosine kinase phosphorylation site:

Amino acids 188-197

N-myristoylation sites:

Amino acids 16-22;89-95;144-150;267-273

Fibrinogen beta and gamma chains C-terminal domain signature:

Amino acids 242-255

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FIGURE 317

CCCAAGCCAGCCGAGCCGCCAGAGCCGCGGGCCGCGGGGGTGTGCGGGGCCCAACCCCAGG**AT**
GCTCCCCCTGCGCCTCCTGCCTACCCGGGTCTCTACTGCTCTGGGCGCTGCTACTGTTGCTCTT
GGGATCAGCTTCTCCTCAGGATTCTGAAGAGCCCGACAGCTACACGGAATGCACAGATGGCTA
TGAGTGGGACCCAGACAGCCAGCACTGCCGGGATGTCAACGAGTGTCTGACCATCCCTGAGGC
CTGCAAGGGGGAAATGAAGTGCATCAACCACTACGGGGGGCTACTTGTGCCTGCCCCGCTCCGC
TGCCGTCATCAACGACCTACATGGCGAGGGACCCCCGCCACCAGTGCCTCCCGCTCAACACCC
CAACCCCTGCCCACCAGGCTATGAGCCCGACGATCAGGACAGCTGTGTGGATGTGGACGAGTG
TGCCAGGGCCCTGCACGACTGTCGCCCCAGCCAGGACTGCCATAACTTGCCTGGCTCCTATCA
GTGCACCTGCCCTGATGGTTACCGCAAGATCGGGCCCCGAGTGTGTGGACATAGACGAGTGCCG
CTACCGCTACTGCCAGACCGCTGCGTGAACCTGCCTGGCTCCTTCCGCTGCCAGTGCAGGCC
GGGCTTCCAGCTGGGGCCTAACAACCGCTCCTGTGTTGATGTGAACGAGTGTGACATGGGGGC
CCCATGCGAGCAGCGCTGCTTCAACTCCTATGGGACCTTCCCTGTGTGCTGCCACCAGGGCTA
TGAGCTGCATCGGGATGGCTTCTCCTGCAGTGATATTGATGAGTGTAGCTACTCCAGCTACCT
CTGTCAGTACCGCTGCGTCAACGAGCCAGGCCGTTTCTCCTGCCACTGCCACAGGGTTACCA
GCTGCTGGCCACACGCCTCTGCCAAGACATTGATGAGTGTGAGTCTGGTGCGCACCAAGTGCCTC
CGAGGGCCCAACCTGTGTCAACTTCCATGGGGGCTACCGCTGCGTGGACACCAACCGCTGCGT
GGAGCCCTACATCCAGGTCTCTGAGAACCGCTGTCTCTGCCCGGCCTCCAACCTCTATGTGCG
AGAGCAGCCTTCATCCATTGTGCACCGCTACATGACCATCACCTCGGAGCGGAGCGTGCCCGC
TGACGTGTTCCAGATCCAGGCGACCTCCGTCTACCCCGGTGCCTACAATGCCTTTCAGATCCG
TGCTGGAAACTCGCAGGGGGACTTTTACATTAGGCAAATCAACAACGTCAGCGCCATGCTGGT
CCTCGCCCCGGCCGGTGACGGGGCCCCCGGGAGTACGTGCTGGACCTGGAGATGGTCACCATGAA
TTCCCTCATGAGCTACCGGGCCAGCTCTGTACTGAGGCTCACCGTCTTTGTAGGGGCCTACAC
CTT**CTGA**GGAGCAGGAGGGAGCCACCCTCCCTGCAGCTACCCTAGCTGAGGAGCCTGTTGTGA
GGGGCAGAATGAGAAAGGCAATAAAGGGAGAAAGAAAGTCTTGGTGGCTGAGGTGGGCGGGTC
ACACTGCAGGAAGCCTCAGGCTGGGGCAGGGTGGCACTTGGGGGGGCAGGCCAAGTTCACCTA
AATGGGGGTCTCTATATGTTTCAGGCCCAGGGGGCCCCCATTTGACAGGAGCTGGGAGCTCTGCAC
CACGAGCTTCAGTCACCCCGAGAGGAGAGGAGGTAACGAGGAGGGCGGACTCCAGGCCCCGGC
CCAGAGATTTGGACTTGGCTGGCTTGCAGGGGTCCTAAGAACTCCACTCTGGACAGCGCCAG
GAGGCCCTGGGTTCATTCTAACTCTGCCTCAAACGTACATTTGGATAAGCCCTAGTAGTT
CCCTGGGCCTGTTTTTCTATAAAACGAGGCAACTGGAAAAAAAAAAAA

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FIGURE 318

MLPCASCLPGSLLLWALLLLLLLGSASPQDSEEPDSYTECTDGYEWDPDSQHCRDVNECLTIPE
ACKGEMKCINHYGGYLCLPRSAAVINDLHGEGPPPPVPPAQHPNPCPPGYEPDDQDSCVDVDE
CAQALHDCRPSQDCHNLPGSYQCTCPDGYRKIGPECVDIDECRYRYCQHRCVNLPGSFRCQCE
PGFQLGPNNRSCVDVNECDMGAPCEQRCFNSYGTFLCRCHQGYELHRDGFSCSDIDECSYSSY
LCQYRCVNEPGRFSCHCPQGYQLLATRLCQDIDECESGAHQCEAQTVCVNFHGGYRCVDTNRC
VEPYIQVSENRCLCPASNPLCREQPSSIVHRYMTITSERSVPADVFIQATSVYPGAYNAFQI
RAGNSQGDFYIRQINNVSAMLVLARPVTGPREYVLDLEMVTMNSLMSYRASSVLRLTVFVGAYTF

Important features:**Signal sequence:**

Amino acids 1-25

N-glycosylation sites:

Amino acids 198-202;394-398

N-myristoylation sites:Amino acids 76-82;145-151;182-188;222-228;290-296;305-311;
371-377;381-387**Aspartic acid and asparagine hydroxylation sites:**

amino acids 140-152;177-189;217-229;258-270

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FIGURE 319

GCTGGGGACATGAGAGGCACACCGAAGACCCACCTCCTGGCCTTCTCCCTCCTCTGCCTCCTC
TCAAAGGTGCGTACCCAGCTGTGCCCCGACACCATGTACCTGCCCCCTGGCCACCTCCCCGATGC
CCGCTGGGAGTACCCCTGGTGCTGGATGGCTGTGGCTGCTGCCGGGTATGTGCACGGCGGCTG
GGGAGCCCTGCGACCAACTCCACGTCTGCGACGCCAGCCAGGGCCTGGTCTGCCAGCCCGGG
GCAGGACCCGGTGGCCGGGGGGCCCTGTGCCTCTTGGCAGAGGACGACAGCAGCTGTGAGGTG
AACGGCCGCCTGTATCGGGAAGGGGAGACCTTCCAGCCCCACTGCAGCATCCGCTGCCGCTGC
GAGGACGGCGGCTTCACCTGCGTGCCGCTGTGCAGCGAGGATGTGCGGCTGCCAGCTGGGAC
TGCCCCACCCCAGGAGGGTCGAGGTCCTGGGCAAGTGCTGCCCTGAGTGGGTGTGCGGCCAA
GGAGGGGGACTGGGGACCCAGCCCCCTTCCAGCCCAAGGACCCCAAGTTTTCTGGCCTTGTCTCT
TCCCTGCCCCCTGGTGTCCCCTGCCCAGAATGGAGCACGGCCTGGGGACCCTGCTCGACCACC
TGTGGGCTGGGCATGGCCACCCGGGTGTCCAACCAGAACCGCTTCTGCCGACTGGAGACCCAG
CGCCGCCTGTGCCTGTCCAGGCCCTGCCCACCCTCCAGGGGTGCGAGTCCACAAAACAGTGCC
TTCTAGAGCCGGGCTGGGAATGGGGACACGGTGTCCACCATCCCCAGCTGGTGGCCCTGTGCC
TGGGCCCTGGGCTGATGGAAGATGGTCCGTGCCAGGCCCTTGGCTGCAGGCAACACTTTAGC
TTGGGTCCACCATGCAGAACACCAATATTAACACGCTGCCTGGTCTGTCTGGATCCCGAGGTA
TGGCAGAGGTGCAAGACCTAGTCCCCTTTCCTCTAACTCACTGCCTAGGAGGCTGGCCAAGGT
GTCCAGGGTCCTCTAGCCCACTCCCTGCCTACACACACAGCCTATATCAAACATGCACACGGG
CGAGCTTCTCTCCGACTTCCCCTGGGCAAGAGATGGGACAAGCAGTCCCTTAATATTGAGGC
TGCAGCAGGTGCTGGGCTGGACTGGCCATTTTTCTGGGGGTAGGATGAAGAGAAGGCACACAG
AGATTCTGGATCTCCTGCTGCCTTTTCTGGAGTTTGTAATAATTGTTCCCTGAATACAAGCCTAT
GCGTGA

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FIGURE 320

MRGTPKTHLLAFSL LCLLSKVRTQLCPTPCTCPWPPPRCPLGVPLVLDGCGCCRV CARRLGEP
CDQLHVCDASQGLVCQPGAGPGGRGALCLLAEDDSSCEVNGRLYREGETFQPHCSIRCRCE DG
GFTCVPLCSEDVRLPSWDCPHPRRVEVLGKCCPEWVCGQGGGLGTQPLPAQGPQFSGLVSSLP
PGVPCPEWSTAWGPCSTTCGLGMATRVSNQNRFCRLETQRR LCLSRPCPPSRGRSPQNSAF

Important features:

Signal sequence:

Amino acids 1-23

N-myristoylation sites:

Amino acids 3-9;49-55;81-87;85-91;126-132;164-170;166-172;

167-173;183-189;209-215

Insulin-like growth factor binding proteins signature:

Amino acids 49-65

von Willebrand C1 domain:

Amino acids 107-124

Thrombospondin 1 Homology Block:

Amino acids 201-216

IGF binding protein site:

Amino acids 49-58

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FIGURE 321

[illegible]

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FIGURE 322

MMGLSLASAVLLASLLSLHLGTATRGSDISKTCFQYSHKPLPWTWVRSYEFTSNSCSQRAVI
FTTKRGKKVCTHPRKKWVQKYISLLKTPKQL

Important features:

Signal peptide:

amino acids 1-23

N-myristoylation sites.

amino acids 3-9, 26-32

Amidation site.

amino acids 68-72

Small cytokines (intecrine/chemokine).

amino acids 23-88

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FIGURE 323

ACCGAGCCGAGCGGACCGAAGGCGCGCCCGAG**ATG**CAGGTGAGCAAGAGGATGCTGGCGGGGGGCGTGAGGAGCA
TGCCAGCCCCCTCCTGGCCTGCTGGCAGCCCATCCTCCTGCTGGTGCTGGGCTCAGTGCTGTGAGGCTCGGCCA
CGGGCTGCCCCGCCCCGCTGCGAGTGCTCCGCCCAGGACCGCGCTGTGCTGTGCCACCGCAAGTGCTTTGTGGCAG
TCCCCGAGGGCATCCCCACCGAGACGCGCCTGCTGGACCTAGGCAAGAACCGCATCAAAACGCTCAACCAGGACG
AGTTCGCCAGCTTCCCGCACCTGGAGGAGCTGGAGCTCAACGAGAACATCGTGAGCGCCGTGGAGCCCGGCGCCT
TCAACAACCTCTTCAACCTCCGGACGCTGGGTCTCCGCAGCAACCGCCTGAAGCTCATCCCGCTAGGCGTCTTCA
CTGGCCTCAGCAACCTGACCAAGCAGGACATCAGCGAGAACAAGATCGTTATCCTACTGGACTACATGTTTCAGG
ACCTGTACAACCTCAAGTCACTGGAGGTTGGCGACAATGACCTCGTCTACATCTCTACCGCGCCTTCAGCGGCC
TCAACAGCCTGGAGCAGCTGACGCTGGAGAAATGCAACCTGACCTCCATCCCCACCGAGGCGCTGTCCACCTGC
ACGGCCTCATCGTCTGAGGCTCCGGCACCTCAACATCAATGCCATCCGGGACTACTCCTTCAAGAGGCTGTACC
GACTCAAGGTCTTGGAGATCTCCCACTGGCCCTACTTGGACACCATGACACCCAAGTGCCTCTACGGCCTCAACC
TGACGTCCCTGTCCATCACACACTGCAATCTGACCGCTGTGCCCTACCTGGCCGTCCGCCACCTAGTCTATCTCC
GCTTCCTCAACCTCTCCTACAACCCCATCAGCACCATTGAGGGCTCCATGTTGCATGAGCTGCTCCGGCTGCAGG
AGATCCAGCTGGTGGGCGGGCAGCTGGCCGTGGTGGAGCCCTATGCCTTCCGCGGCCTCAACTACCTGCGCGTGC
TCAATGTCTCTGGCAACCAGCTGACCACACTGGAGGAATCAGTCTTCCACTCGGTGGGCAACCTGGAGACACTCA
TCCTGGACTCCAACCCGCTGGCCTGCGACTGTGCGCTCCTGTGGGTGTTCCGGCGCCGCTGGCGGCTCAACTTCA
ACGGGCAGCAGCCACGTGCGCCACGCCCCAGTTTGTCCAGGGCAAGGAGTTCAAGGACTTCCCTGATGTGCTAC
TGCCCAACTACTTACCTGCCGCGCGCCCCGCATCCGGGACCGCAAGGCCAGCAGGTGTTTGTGGACGAGGGCC
ACACGGTGCAGTTTGTGTGCCGGGCGCGATGGCGACCCGCCGCCCATCCTCTGGCTCTACCCCGAAAGCACC
TGGTCTCAGCCAAGAGCAATGGGCGGCTCACAGTCTTCCCTGATGGCACGCTGGAGGTGCGCTACGCCCAGGTAC
AGGACAACGGCACGTACCTGTGCATCGCGGCCAACGCGGGCGGCAACGACTCCATGCCCGCCCACCTGCATGTGC
GCAGCTACTCGCCCGACTGGCCCCATCAGCCCAACAAGACCTTCGCTTTCATCTCCAACCAGCCGGGCGAGGGAG
AGGCCAACAGCACC CGCGCCACTGTGCCTTTCCCTTTCGACATCAAGACCCTCATCATCGCCACCACCATGGGCT
TCATCTCTTTCCCTGGGCGTCTCCTCTTCTGCCTGGTGCTGCTGTTTCTCTGGAGCCGGGGCAAGGGCAACACAA
AGCACAACATCGAGATCGAGTATGTGCCCCGAAAGTCGGACGCAGGCATCAGCTCCGCCGACGCGCCCCGCAAGT
TCAACATGAAGATGATA**TGA**GGCCGGGGCGGGGGCAGGGACCCCCGGGCGGCCGGGCAGGGGAAGGGGCGCTGGT
CGCCACCTGCTCACTCTCCAGTCTTCCCACCTCCTCCCTACCTTCTACACACGTTCTCTTTCTCCCTCCCGCC
TCCGTCCCCTGCTGCCCCCGCCAGCCCTCACCACCTGCCCTCCTTCTACCAGGACCTCAGAAGCCCAGACCTGG
GGACCCACCTACACAGGGGCATTGACAGACTGGAGTTGAAAGCCGACGAACCGACACGCGGCAGAGTCAATAAT
TCAATAAAAAAGTTACGAACCTTCTCTGTAACCTGGGTTTCAATAATTATGGATTTTATGAAAACCTTGAAATAA
TAAAAAGAGAAAAAACTAAAAAAAAAAAAAAAAAAAAA

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FIGURE 324

MQVSKRMLAGGVSRMPSPLLACWQPILLVLGSLVSGSATGCPPRCECSAQDRAVLCHRKCFVAVPEGIPTETRL
LDLGKNRIKTLNQDEFASFPHLEELNENIVSAVEPGAFFNNLFNLRITLGLRSNRLKLIPLGVFTGLSNLTKQDI
SENKIVILLDYMFDLYNLKSLEVGDNDLVYISHRAFSGLSLEQLTLEKCNLTSIPTEALSHLHGLIVLRLRHL
NINAIRDYSFKRLYRLKVLEISHWPYLDTMTPNCLYGLNLTSLSITHCNLTAVPYLAVRHLVYLRFLNLSYNPIS
TIEGSMHELLRLQEIQLVGGQLAVVEPYAFRGLNYLRVLNVSGNQLTLEESVFHSGVGNLETILDSNPLACDC
RLLWVFRRRWRLNFNRRQPTCATPEFVQGKEFKDFPDVLLPNYFTCRRARIRDRKAQQVFVDEGHTVQFVCRADG
DPPPAIWLSPRKHLVSAKSNRGLTVFPDGTLEVRYAQVQDNGTYLCIAANAGGNDMPAHLHVRSYSPDWPHQP
NKTFAFISNQPGEGEANSTRATVPFPFDIKTLIIATTMGFISFLGVVLFCLVLLFLWSRGKGNTKHNIEIEYVPR
KSDAGISSADAPRKFNMKMI

Important features:**Signal sequence:**

amino acids 1-41

Transmembrane domain:

amino acids 556-578

N-glycosylation site.amino acids 144-148, 202-206, 264-268, 274-278, 293-297, 341-345, 492-496,
505-509, 526-530, 542-546**Casein kinase II phosphorylation site.**

amino acids 49-53, 108-112, 146-150, 300-304, 348-352, 349-353, 607-611

Tyrosine kinase phosphorylation site.

amino acids 590-598

N-myristoylation site.amino acids 10-16, 32-38, 37-43, 113-119, 125-131, 137-143, 262-268, 320-326,
344-350, 359-365, 493-499, 503-509, 605-611**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 32-43

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FIGURE 325

CCCACGCGTCCGCCCACGCGTCCGAGGGACAAGAGAGAAGAGAGACTGAAACAGGGAGAAGAG
GCAGGAGAGGAGGAGGTGGGGAGAGCACGAAGCTGGAGGCCGACACTGAGGGAGGGCGGGAGG
AGGTGAAGAAGGAGAGAGGGGAGAAGAGGCAGGAGCTGGAAAGGAGAGAGGGAGGAGGAGGAG
GAGATGCGGGATGGAGACCTGGAGTTAGGTGGCTTGGGAGAGCTTAATGAAAAGAGAACGGAG
AGGAGGTGTGGGTTAGGAACCAAGAGGTAGCCCTGTGGGCAGCAGAAGGCTGAGAGGAGTAGG
AAGATCAGGAGCTAGAGGGAGACTGGAGGGTTCCGGGAAAAGAGCAGAGGAAAGAGGAAAGAC
ACAGAGAGACGGGAGAGAGAAGAAGAGTGGGTTTGAAGGGCGGATCTCAGTCCCTGGCTGCTT
TGGCATTGTTGGGAACTGGGACTCCCTGTGGGGAGGAGAGGAAAGCTGGAAGTCCTGGAGGGAC
AGGGTCCCAGAAGGAGGGGACAGAGGAGCTGAGAGAGGGGGGCAGGGCGTTGGGCAGGGGTCC
CTCGGAGGCCTCCTGGGGATGGGGGCTGCAGCTCGTCTGAGCGCCCCTCGAGCGCTGGTACTC
TGGGCTGCACTGGGGGCAGCAGCTCACATCGGACCAGCACCTGACCCCGAGGACTGGTGGAGC
TACAAGGATAATCTCCAGGGAACTTCGTGCCAGGGCCTCCTTTCTGGGGCCTGGTGAATGCA
GCGTGGAGTCTGTGTGCTGTGGGGAAGCGGCAGAGCCCCGTGGATGTGGAGCTGAAGAGGGTT
CTTTATGACCCCTTTCTGCCCCATTAAAGGCTCAGCACTGGAGGAGAGAAGCTCCGGGGAAACC
TTGTACAACACCGGCCGACATGTCTCCTTCCTGCCTGCACCCCGACCTGTGGTCAATGTGTCT
GGAGGTCCCCTCCTTTACAGCCACCGACTCAGTGAAGTGC GGCTGCTGTTTGGAGCTCGCGAC
GGAGCCGGCTCGGAACATCAGATCAACCACCAGGGCTTCTCTGCTGAGGTGCAGCTCATTAC
TTCAACCAGGAAGTCTACGGGAATTTACAGCGCTGCCTCCCGCGGCCCAATGGCCTGGCCATT
CTCAGCCTCTTTGTCAACGTTGCCAGTACCTCTAACCCTCCTCAGTCGCCTCCTTAACCGC
GACACCATCACTCGCATCTCCTACAAGAATGATGCCTACTTTCTTCAAGACCTGAGCCTGGAG
CTCCTGTTCCCTGAATCCTTCGGCTTCATCACCTATCAGGGCTCTCTCAGCACCCCGCCCTGC
TCCGAGACTGTCACCTGGATCCTCATTGACCGGGCCCTCAATATCACCTCCCTTCAGATGCAC
TCCCTGAGACTCCTGAGCCAGAATCCTCCATCTCAGATCTTCCAGAGCCTCAGCGGTAACAGC
CGGCCCCCTGCAGCCCTTGGCCCACAGGGCACTGAGGGGCAACAGGGACCCCCGGCACCCCGAG
AGGCGCTGCCGAGGCCCAACTACCGCCTGCATGTGGATGGTGTCCCCCATGGTCGCTGAAGAC
TCCCCTTCGAGGATTGCACCCGCCCGTCCTAAGCCTCCCCACAAGGCGAGGGGAGTTACCCCT
AAAACAAAGCTATTAAAGGGACAGAATACTTA

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FIGURE 326

MGAAARLSAPRALVLWAALGAAAHIGPAPDPEDWWSYKDNLQGNFVPGPPFWGLVNAAWSLCA
VGKRQSPVDVELKRVLYDPFLPPLRLSTGGEKLRGTLYNTGRHVSFLPAPRPVVNVSGGPLY
SHRLSELRLFLFGARDGAGSEHQINHQGFSAEVQLIHFNQELYGNFSAASRGPNGLAILSLFVN
VASTSNPFLSRLLNRDTITRISYKNDAYFLQDLSLELLFPESFGFITYQGSLSTPPCSETVTW
ILIDRALNITSLQMHSRLRLSQNPFSQIFQSLSGNSRPLQPLAHRALRGNRDPRHPERRCRGP
NYRLHVDGVPHGR

Important features:**Signal peptide:**

Amino acids 1-23

Transmembrane domain:

Amino acids 177-199

N-glycosylation sites:

Amino acids 118-122;170-174;260-264

Eukaryotic-type carbonic anhydrases proteins:

Amino acids 222-271;128-165;45-93

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FIGURE 327

GGACTAATCTGTGGGAGCAGTTTATTCCAGTATCACCCAGGGTGCAGCCACACCAGGACTGTGTTGAAGGGTGT
TTTTTTCTTTTAAATGTAATACCTCCTCATCTTTTCTTCTTACACAGTGTCTGAGAACATTTACATTATAGATAA
GTAGTACATGGTGGATAACTTCTACTTTTAGGAGGACTACTCTCTTCTGACAGTCCTAGACTGGTCTTCTACACT
AAGACACCATGAAGGAGTATGTGCTCCTATTATTCTGCTTTGTGCTCTGCCAAACCCTTCTTTAGCCCTTCAC
ACATCGCACTGAAGAATATGATGCTGAAGGATATGGAAGACACAGATGATGATGATGATGATGATGATGATGATG
ATGATGATGAGGACAACCTCTCTTTTCCAACAAGAGAGCCAAGAAGCCATTTTTTTCCATTTGATCTGTTTCCAA
TGTGTCCATTTGGATGTCAGTGCTATTACGAGTTGTACATTGCTCAGATTTAGGTTTGACCTCAGTCCCAACCA
ACATTCCATTTGATACTCGAATGCTTGATCTTCAAAACAATAAAATTAAGGAAATCAAAGAAAATGATTTTAAAG
GACTCACTTCACCTTATGGTCTGATCCTGAACAACAACAAGCTAACGAAGATTCACCCAAAAGCCTTTCTAACCA
CAAAGAAGTTGCGAAGGCTGTATCTGTCCCACAATCAACTAAGTGAAATACCACTTAATCTTCCCAAATCATTAG
CAGAACTCAGAATTCATGAAAATAAAGTTAAGAAAATACAAAAGGACACATTCAAAGGAATGAATGCTTTACACG
TTTTGGAAATGAGTGCAAACCCTCTTGATAATAATGGGATAGAGCCAGGGGCATTTGAAGGGGTGACGGTGTTC
ATATCAGAATTGCAGAAGCAAACTGACCTCAGTTCCTAAAGGCTTACCACCACTTTATTGGAGCTTCACTTAG
ATTATAATAAAATTTCAACAGTGGAACCTTGAGGATTTTAAACGATACAAAGAATAACAAAGGCTGGGCCTAGGAA
ACAACAAAATCACAGATATCGAAAATGGGAGTCTTGCTAACATACCACGTGTGAGAGAAATACATTTGGAAAACA
ATAAACTAAAAAAATCCCTTCAGGATTACCAGAGTTGAAATACCTCCAGATAATCTTCTTCATTCTAATTCAA
TTGCAAGAGTGGGAGTAAATGACTTCTGTCCAACAGTGCCAAAGATGAAGAAATCTTTATACAGTGCAATAAGTT
TATTCAACAACCCGGTGAAATACTGGGAAATGCAACCTGCAACATTTTCGTTGTGTTTTGAGCAGAATGAGTGTTT
AGCTTGGGAACCTTTGGAATGTAATAATTAGTAATTGGTAATGTCCATTTAATATAAGATTCAAAAATCCCTACAT
TTGGAATACTTGAACCTCTATTAATAATGGTAGTATTATATATACAAGCAAATATCTATTCTCAAGTGGAAGTCC
ACTGACTTATTTTATGACAAGAAATTTCAACGGAATTTTGCCAACTATTGATACATAAGGGGTGAGAGAAAACA
AGCATCTATTGCAGTTTTCTTTTTGCGTACAAATGATCTTACATAAAATCTCATGCTTGACCATTCCTTTCTTCAT
AACAAAAAGTAAGATATTCGGTATTTAACACTTTGTTATCAAGCACATTTTAAAAAGAACTGTACTGTAAATGG
AATGCTTGACTTAGCAAAATTTGTGCTCTTTCATTTGCTGTTAGAAAAACAGAATTAACAAAGACAGTAATGTGA
AGAGTGCATTACACTATTCTTATCTTTAGTAACTTGGGTAGTACTGTAATATTTTAAATCATCTTAAAGTATGA
TTTGATATAATCTTATTGAAATTACCTTATCATGTCTTAGAGCCCGTCTTTATGTTTAAACTAATTTCTTAAAA
TAAAGCCTTCAGTAAATGTTTATTACCAACTTGATAAATGCTACTCATAAGAGCTGGTTTGGGGCTATAGCATAT
GCTTTTTTTTTTTTAAATTATTACCTGATTTAAAAATCTCTGTAAAAACGTGTAGTGTTTCATAAAATCTGTAAC
CGCATTTTAAATGATCCGCTATTATAAGCTTTTAAATAGCATGAAAATGTTAGGCTATATAACATTGCCACTTCAA
CTCTAAGGAATATTTTTGAGATATCCCTTTGGAAGACCTTGCTTGGAAGAGCCTGGACACTAACAAATCTACACC
AAATTGTCTCTTCAAATACGTATGGACTGGATAACTCTGAGAAACACATCTAGTATAACTGAATAAGCAGAGCAT
CAAATTAAACAGACAGAAACCGAAAGCTCTATATAAATGCTCAGAGTTCTTTATGTATTTCTTATTGGCATTCAA
CATATGTAAATCAGAAAACAGGGAAATTTTCATTAAAAATATTGGTTGAAAT

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FIGURE 328

MKEYVLLLFLALCSAKPFFSPSHIALKNMMLKDMEDTDDDDDDDDDDDDDDDEDNSLFPTREPRS
HFFPFDLFPMCPFGCQCYSRVVHCSDLGLTSVPTNIPFDTRMLDLQNNKIKEIKENDFKGLTS
LYGLILNNNKLTKIHPKAFLTTKKLRRLYLSHNQLSEIPLNLPKSLAELRIHENKVKKIQKDT
FKGMNALHVLEMSANPLDNNGIEPGAFEGVTVFHIRIAEAKLTSVPKGLPPTLLELHLDYNKI
STVELEDFKRYKELQRLGLGNNKITDIENGLANIPRVREIHLENNKLKKIPSGLPPELKYLQI
IFLHSNSIARVGVNDFCPTVPKMKKSLYSAISLFNNPVKYWEMQPATFRCVLSRMSVQLGNFGM

Important features:**Signal sequence.**

amino acids 1-15

N-glycosylation site.

amino acids 281-285

N-myristoylation sites.

amino acids 129-135, 210-216, 214-220, 237-243, 270-276, 282-288

Leucine zipper pattern.

amino acids 154-176

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FIGURE 329

GGGGTCTCCCTCAGGGCCGGGAGGCACAGCGGTCCCTGCTTGCTGAAGGGCTGGATGTACGCA
TCCGCAGGTTCCCGCGGACTTGGGGGCGCCCGCTGAGCCCCGGCGCCCGCAGAAGACTTGTGT
TTGCCTCCTGCAGCCTCAACCCGGAGGGCAGCGAGGGCCTACCACC**ATG**ATCACTGGTGTGTT
CAGCATGCGCTTGTGGACCCAGTGGGCGTCCTGACCTCGCTGGCGTACTGCCTGCACCAGCG
GCGGGTGGCCCTGGCCGAGCTGCAGGAGGCCGATGGCCAGTGTCCGGTCGACCGCAGCCTGCT
GAAGTTGAAAATGGTGCAGGTCGTGTTTCGACACGGGGCTCGGAGTCCTCTCAAGCCGCTCCC
GCTGGAGGAGCAGGTAGAGTGGAACCCCCAGCTATTAGAGGTCCCACCCCAAACCTCAGTTTGA
TTACACAGTCACCAATCTAGCTGGTGGTCCGAAACCATATTCTCCTTACGACTCTCAATACCA
TGAGACCACCTGAAGGGGGGCATGTTTGCTGGGCAGCTGACCAAGGTGGGCATGCAGCAAAT
GTTTGCCTTGGGAGAGAGACTGAGGAAGAACTATGTGGAAGACATTCCTTTCTTTACCAAC
CTTCAACCCACAGGAGGTCTTTATTCGTTCCACTAACATTTTTCGGAATCTGGAGTCCACCCG
TTGTTTGCTGGCTGGGCTTTTCCAGTGTGAGAAAGAACGACCCATCATCATCCACACTGATGA
AGCAGATTCAGAAGTCTTGATCCCAACTACCAAAGCTGCTGGAGCCTGAGGCAGAGAACCAG
AGGCCGGAGGCAGACTGCCTCTTTACAGCCAGGAATCTCAGAGGATTTGAAAAGGTGAAGGA
CAGGATGGGCATTGACAGTAGTGATAAAGTGGACTTCTTCATCCTCCTGGACAACGTGGCTGC
CGAGCAGGCACACAACCTCCCAAGCTGCCCCATGCTGAAGAGATTTGCACGGATGATCGAACA
GAGAGCTGTGGACACATCCTTGATACATACTGCCAAGGAAGACAGGGAAAGTCTTCAGATGGC
AGTAGGCCCATTCCTCCACATCCTAGAGAGCAACCTGCTGAAAGCCATGGACTCTGCCACTGC
CCCCGACAAGATCAGAAAGCTGTATCTCTATGCGGCTCATGATGTGACCTTCATACCGCTCTT
AATGACCCTGGGGATTTTTGACCACAAATGGCCACCGTTTGCTGTTGACCTGACCATGGAAC
TTACCAGCACCTGGAATCTAAGGAGTGGTTTGTGCAGCTCTATTACCACGGGAAGGAGCAGGT
GCCGAGAGGTTGCCCTGATGGGCTCTGCCCGCTGGACATGTTCTTGAATGCCATGTCAGTTTA
TACCTTAAGCCCAGAAAAATACCATGCACTCTGCTCTCAAACCTCAGGTGATGGAAGTTGGAAA
TGAAGAG**TAA**CTGATTTATAAAAGCAGGATGTGTTGATTTTAAAATAAAGTGCCTTTATACAATG

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FIGURE 330

MITGVFSMRLWTPVGVLTSLAYCLHQRRVALAELQEADGQCPVDRSLLKLMVQVVFRHGARSPLKPLPLEEQVE
WNPQLLEVPPQTQFDYTVTNLAGGPKPYSPYDSQYHETTLKGGMFAGQLTKVGMQQMFALGERLRKNYVEDIPFL
SPTFNPQEVFIRSTNIFRNLESTRCLLAGLFQCQKEGPIIIHTDEADSEVLYPNYQSCWSLRQRTGRRRQTASLQ
PGISEDLLKKVKDRMGIDSSDKVDFFILLDNVAAEQAHNLPSCPMLKR FARMIEQRAVDTSLYILPKEDRESLQMA
VGPFLHILES NLLKAMDSATAPDKIRKLYLYAAHDVTFIPLMLTLGIFDHKWPPFÄVDLTMELYQHLESKEWFVQ
LYYHGKEQVPRGCPDGLCPLDMFLNAMS VYTLSP EKYHALCSQTQVMEVGNEE

Important features:**Signal sequence:**

amino acids 1-23

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 218-222

Casein kinase II phosphorylation site.

amino acids 87-91, 104-108, 320-324

Tyrosine kinase phosphorylation site.

amino acids 280-288

N-myristoylation site.

amino acids 15-21, 117-123, 118-124, 179-185, 240-246, 387-393

Amidation site.

amino acids 216-220

Leucine zipper pattern.

amino acids 10-32

Histidine acid phosphatases phosphohistidine signature.

amino acids 50-65

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FIGURE 331

CGAGGGCTTTTCCGGCTCCGGAATGGCACATGTGGGAATCCCAGTCTTGTTGGCTACAACATTTTCCCTTTCCT
AACAAAGTTCTAACAGCTGTTCTAACAGCTAGTGATCAGGGGTCTTCTTGCTGGAGAAGAAAGGGCTGAGGGCAG
AGCAGGGCACTCTCACTCAGGGTGACCAGCTCCTTGCCCTCTCTGTGGATAACAGAGCATGAGAAAGTGAAGAGAT
GCAGCGGAGTGAGGTGATGGAAGTCTAAAATAGGAAGGAATTTTGTGTGCAATATCAGACTCTGGGAGCAGTTGA
CCTGGAGAGCCTGGGGGAGGGCCTGCCTAACAAAGCTTTCAAAAAACAGGAGCGACTTCCACTGGGCTGGGATAAG
ACGTGCCGGTAGGATAGGGAAGACTGGGTTTAGTCTTAATATCAAATTGACTGGCTGGGTGAACTTCAACAGCCT
TTTAACCTCTCTGGGAGATGAAAACGATGGCTTAAGGGGCCAGAAATAGAGATGCTTTGTAAAATAAAATTTTAA
AAAAAGCAAGTATTTTATAGCATAAAGGCTAGAGACCAAAATAGATAACAGGATTCCCTGAACATTCTTAAGAGG
GAGAAAGTATGTTAAAAATAGAAAAACCAAAATGCAGAAGGAGGAGACTCACAGAGCTAAACCAGGATGAGGGGACC
CTGGGTGAGGCCAGCCTCTTTGCTCCTCCCGGAAATTATTTTGGTCTGACCACTCTGCCTTGTGTTTTGCAGAA
TCATGTGAGGGCCAACCGGGGAAGGTGGAGCAGATGAGCACACACAGGAGCCGTCTCCTCACCGCCGCCCTCTC
AGCATGGAACAGAGGCAGCCCTGGCCCCGGGCCCTGGAGGTGGACAGCCGCTCTGTGGTCTGCTCTCAGTGGTC
TGGGTGCTGCTGGCCCCCAGCAGCCGGCATGCCTCAGTTCAGCACCTTCCACTCTGAGAATCGTGACTGGACC
TTCAACCACTTGACCGTCCACCAAGGGACGGGGGCCGTCTATGTGGGGGCCATCAACCGGGTCTATAAGCTGACA
GGCAACCTGACCATCCAGGTGGCTCATAAGACAGGGCCAGAAGAGGACAACAAGTCTCGTTACCCGCCCTCATC
GTGCAGCCCTGCAGCGAAGTGCTCACCTCACCAACAATGTCAACAAGCTGCTCATCATTGACTACTCTGAGAAC
CGCCTGCTGGCCTGTGGGAGCCTCTACCAGGGGTCTGCAAGCTGCTGCGGCTGGATGACCTCTTCATCCTGGTG
GAGCCATCCCAAGAAGGAGCACTACCTGTCCAGTGTCAACAAGACGGGCACCATGTACGGGGTGATTGTGCGC
TCTGAGGGTGAGGATGGCAAGCTCTTCATCGGCACGGCTGTGGATGGGAAGCAGGATTACTTCCCGACCTGTCC
AGCCGGAAGCTGCCCCGAGACCCTGAGTCTCAGCCATGCTCGACTATGAGCTACACAGCGATTTTGTCTCCTCT
CTCATCAAGATCCCTTCAGACACCCTGGCCCTGGTCTCCCACTTTGACATCTTCTACATCTACGGCTTTGCTAGT
GGGGGCTTTGTCTACTTTCTCACTGTCCAGCCGAGACCCCTGAGGGTGTGGCCATCAACTCCGCTGGAGACCTC
TTCTACACCTCACGCATCGTGCGGCTCTGCAAGGATGACCCCAAGTTCCTACTCATACGTGTCCCTGCCCTTCGGC
TGCACCCGGGCCGGGTGGAATACCGCCTCCTGCAGGCTGCTTACCTGGCCAAGCCTGGGGACTCACTGGCCCAG
GCCTTCAATATCACCAGCCAGGACGATGTACTCTTTGCCATCTTCTCCAAAGGGCAGAAGCAGTATCACCACCCG
CCCGATGACTCTGCCCTGTGTGCCTTCCCTATCCGGGCCATCAACTTGAGATCAAGGAGCGCCTGCAGTCCCTGC
TACCAGGGCGAGGGCAACCTGGAGCTCAACTGGCTGCTGGGGAAGGACGTCCAGTGCACGAAGGCGCCTGTCCCC
ATCGATGATAACTTCTGTGGACTGGACATCAACCAGCCCTGGGAGGCTCAACTCCAGTGGAGGGCCTGACCCTG
TACACCACAGCAGGGACCGCATGACCTCTGTGGCCTCCTACGTTTACAACGGCTACAGCGTGGTTTTTGTGGGG
ACTAAGAGTGGCAAGCTGAAAAAGGTAAGAGTCTATGAGTTTCAAGATGCTCCAATGCCATTACCTCCTCAGCAAA
GAGTCCCTCTTGGAAGGTAGCTATTGGTGGAGATTTAACTATAGGCAACTTTATTTTCTTGGGGAACAAAGGTGA
AATGGGGAGGTAAGAAGGGTTAATTTTGTGACTTAGCTTCTAGCTACTTCCCTCCAGCCATCAGTCATTGGGTAT
GTAAGGAATGCAAGCGTATTTCAATATTTCCCAAACCTTTAAGAAAAAAGTTAAGAAGGTACATCTGCAAAAGCAAA

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FIGURE 332

MGTLGQASLFAPPGNYFWSHDHSAFCFAESCEGQPGKVEQMSTHRSRLLTAAPLSMEQRQPWPR
ALEVDSRSVLLSVVWVLLAPPAAGMPQFSTFHSENRDWTFNHLTVHQGTGAVYVGAINRVYK
LTGNLTIQVAHKTGPEEDNKSRYPPPLIVQPCSEVLTLTNNVNKLLIIDYSENRLACGSLYQG
VCKLLRLDDLFIIVEPSHKKEHYLSSVNKTGTMYGVIVRSEGEDGKLFIGTAVDGKQDYFPTL
SSRKLPRDPRESSAMLDYELHSDFVSSLIKIPSDTLALVSHFDIFYIYGFASSGGFVYFLTQPE
TPEGVAINSAGDLFYTSRIVRLCKDDPKFHSYVSLPFGCTRAGVEYRLLQAAYLAKPGDSLQ
AFNITSQDDVLFAIFSKGQKQYHHPPDDSALCAFPIRAİNLQIKERLQSCYQGEKNLELNWLL
GKDVQCTKAPVPIDDNFCGLDINQPLGGSTPVEGLTLYTTSRDRMTSVASYVYNGYSVVFVGT
KSGKLKKVRVYEFRCSSNAIHLLSKESLLEGSYWWRFNRYRLYFLGEQR

Important features:**Signal sequence:**

amino acids 1-32

Transmembrane domain:

amino acids 71-87

N-glycosylation site.

amino acids 130-134, 145-149, 217-221, 381-385

Casein kinase II phosphorylation site.amino acids 139-143, 229-233, 240-244, 291-295, 324-328, 383-387,
384-388, 471-475, 481-485, 530-534**N-myristoylation site.**

amino acids 220-226, 319-325, 353-359, 460-466, 503-509

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FIGURE 333

GCTGAGTCTGCTGCTCCTGCTGCTGCTGCTCCAGCCTGTAACTGTGCCTACACCACGCCAGG
CCCCCCCAGAGCCCTCACCACGCTGGGCGCCCCAGAGCCCACACC**ATG**CCGGGCACCTACGC
TCCCTCGACCACACTCAGTAGTCCCAGCACCCAGGGCCTGCAAGAGCAGGCACGGGCCCTGAT
GCGGGACTTCCCGCTCGTGGACGGCCACAACGACCTGCCCCTGGTCCTAAGGCAGGTTTACCA
GAAAGGGCTACAGGATGTTAACCTGCGCAATTTAGCTACGGCCAGACCAGCCTGGACAGGCT
TAGAGATGGCCTCGTGGGCGCCAGTTCTGGTCAGCCTATGTGCCATGCCAGACCCAGGACCG
GGATGCCCTGCGCCTCACCTGGAGCAGATTGACCTCATACGCCGCATGTGTGCCTCCTATTC
TGAGCTGGAGCTTGTGACCTCGGCTAAAGCTCTGAACGACACTCAGAAATTGGCCTGCCTCAT
CGGTGTAGAGGGTGGCCACTCGCTGGACAATAGCCTCTCCATCTTACGTACCTTCTACATGCT
GGGAGTGCCTACCTGACGCTCACCCACACCTGCAACACACCCTGGGCAGAGAGCTCCGCTAA
GGGCGTCCACTCCTTCTACAACAACATCAGCGGGCTGACTGACTTTGGTGAGAAGGTGGTGGC
AGAAATGAACCGCCTGGGCATGATGGTAGACTTATCCCATGTCTCAGATGCTGTGGCACGGCG
GGCCCTGGAAGTGTACAGGCACCTGTGATCTTCTCCCACTCGGCTGCCCCGGGGTGTGTGCAA
CAGTGCTCGGAATGTTCTGATGACATCCTGCAGCTTCTGAAGAAGAACGGTGGCGTCGTGAT
GGTGTCTTTGTCCATGGGAGTAATACAGTGCAACCCATCAGCCAATGTGTCCACTGTGGCAGA
TCACTTCGACCACATCAAGGCTGTCATTGGATCCAAGTTCATCGGGATTGGTGGAGATTATGA
TGGGGCCGGCAAATTCCCTCAGGGGCTGGAAGACGTGTCCACATACCCGGTCCTGATAGAGGA
GTTGCTGAGTCGTGGCTGGAGTGAGGAAGAGCTTCAGGGTGTCTTCGTGGAAACCTGCTGCG
GGTCTTCAGACAAGTGGAAAAGGTACAGGAAGAAAACAAATGGCAAAGCCCCTTGGAGGACAA
GTTCCCGGATGAGCAGCTGAGCAGTTCCTGCCACTCCGACCTCTCACGTCTGCGTCAGAGACA
GAGTCTGACTTCAGGCCAGGAACTCACTGAGATTCCCATACACTGGACAGCCAAGTTACCAGC
CAAGTGGTCAGTCTCAGAGTCCTCCCCCACATGGCCCCAGTCCTTGCAGTTGTGGCCACCTT
CCCAGTCCTTATTCTGTGGCTC**TGA**TGACCCAGTTAGTCCTGCCAGATGTCACTGTAGCAAGC
CACAGACACCCACAAAGTTCCCCTGTTGTGCAGGCACAAATATTTCTGAAATAAATGTTTT
GGACATAG

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FIGURE 334

MPGTYAPSTTLSSPSTQGLQEQARALMRDFPLVDGHNDLPLVLRQVYQKGLQDVNLRNFSYGQ
TSLDRLRDGLVGAQFWSAYVPCQTQDRDALRLTLEQIDLIIRMCASYSELELVTSAKALNDTQ
KLACLIGVEGGHSLDNSLSILRTFYMLGVRYLTLTHTCNTPWAESSAKGVHSFYNNISGLTDF
GEKVVAEMNRLGMMVDLSHVSDAVARRALEVSQAPVIFSHSAARGVCNSARNVPDDILQLLKK
NGGVVMVSLSMGVIQCNPSANVSTVADHFDHIKAVIGSKFIGIGGDYDGAGKFPQGLEDVSTY
PVLIEELLSRGWSEEELQGVLRGNLLRVFRQVEKVQEENKWQSPLEDKFPDEQLSSSCHSDLS
RLRQRQSLTSGQELTEIPIHWTAKLPKWSVSESSPHMAPVLAVVATFPVLILWL

Important features:**N-glycosylation sites.**

amino acids 58-62, 123-127, 182-186, 273-277

N-myristoylation sites.

amino acids 72-78, 133-139, 234-240, 264-270, 334-340, 389-395

Renal dipeptidase active site.

amino acids 134-157

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FIGURE 335

CCCAGAAGTTCAAGGGCCCCCGGCCTCCTGCGCTCCTGCCGCCGGGACCCCTCGACCTCCTCAG
AGCAGCCGGCTGCCGCCCCGGGAAG**ATG**GCGAGGAGGAGCCGCCACCGCCTCCTCCTGCTGCT
GCTGCGCTACCTGGTGGTCGCCCTGGGCTATCATAAGGCCTATGGGTTTTCTGCCCCAAAAGA
CCAACAAGTAGTCACAGCAGTAGAGTACCAAGAGGCTATTTTAGCCTGCAAAACCCCAAAGAA
GACTGTTTTCTCCAGATTAGAGTGGAAGAACTGGGTTCGGAGTGTCTCCTTTGTCTACTATCA
ACAGACTCTTCAAGGTGATTTTAAAAATCGAGCTGAGATGATAGATTTCAATATCCGGATCAA
AAATGTGACAAGAAGTGATGCCGGGAAATATCGTTGTGAAGTTAGTGCCCCATCTGAGCAAGG
CCAAAACCTGGAAGAGGATACAGTCACTCTGGAAGTATTAGTGGCTCCAGCAGTTCCATCATG
TGAAGTACCCTCTTCTGCTCTGAGTGGAAGTGTGGTAGAGCTACGATGTCAAGACAAAGAAGG
GAATCCAGCTCCTGAATACACATGGTTTAAAGGATGGCATCCGTTTGCTAGAAAATCCCAGACT
TGGCTCCCAAAGCACCAACAGCTCATACACAATGAATACAAAACCTGGAAGTCTGCAATTTAA
TACTGTTTCCAAACTGGACACTGGAGAATATTCCTGTGAAGCCCGCAATTCTGTTGGATATCG
CAGGTGTCCTGGGAAACGAATGCAAGTAGATGATCTCAACATAAGTGGCATCATAGCAGCCGT
AGTAGTTGTGGCCTTAGTGATTTCCGTTTGTGGCCTTGGTGTATGCTATGCTCAGAGGAAAGG
CTACTTTTCAAAAGAAACCTCCTTCCAGAAGAGTAATTCTTCATCTAAAGCCACGACAATGAG
TGAAAATGTGCAGTGGCTCACGCCTGTAATCCCAGCACTTTGGAAGGCCGCGGGCGGGCGGATC
ACGAGGTCAGGAGTTCT**TAG**ACCAGTCTGGCCAATATGGTGAAACCCCATCTCTACTAAAATAC
AAAAATTAGCTGGGCATGGTGGCATGTGCCTGCAGTTCCAGCTGCTTGGGAGACAGGAGAATC
ACTTGAACCCGGGAGGCGGAGGTTGCAGTGAGCTGAGATCACGCCACTGCAGTCCAGCCTGGG
TAACAGAGCAAGATTCCATCTCAAAAAATAAAATAAATAAATAAATAAATAAATACTGGTTTTTACC
TGTAGAATTCTTACAATAAATATAGCTTGATATTC

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FIGURE 336

MARRSRHRLLLLLLRYLVVALGYHKAYGFSAPKDQQVVTAVEYQEAILACKTPKKTVSSRLEW
KKLGRSVSFVYYQOTLQGDFKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQGQNLEEDTV
TLEVLVAPAVPSCEVPSSALSGTVVELRCQDKEGNPAPEYTWFKDGIRLLENPRLGSQSTNSS
YTMNTKTGTLQFNTVSKLDTGEYSCEARNSVGYYRRCPGKRMQVDDLNISGIIAAVVVVALVIS
VCGLGVCYAQRKGYFSKETSFQKSNSSSKATTMSENVQWLTPVIPALWKAAAGGSRGQEF

Important features:**Signal peptide:**

amino acids 1-20

Transmembrane domain:

amino acids 130-144, 238-258

N-glycosylation site.

amino acids 98-102, 187-191, 236-240, 277-281

Casein kinase II phosphorylation site.

amino acids 39-43, 59-63, 100-104, 149-153, 205-209, 284-288

N-myristoylation site.

amino acids 182-188, 239-245, 255-261, 257-263, 305-311

Amidation site.

amino acids 226-230

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FIGURE 337

GGAGCCGCCCTGGGTGTCAGCGGCTCGGCTCCCGCGCACGCTCCGGCCGTCGCGCAGCCTCGG
CACCTGCAGGTCCGTGCGTCCCGCGGCTGGCGCCCCTGACTCCGTCCCGGCCAGGGAGGGCCA
TGATTTCCCTCCCGGGGCCCCTGGTGACCAACTTGCTGCGGTTTTTGTTCCTGGGGCTGAGTG
CCCTCGCGCCCCCCTCGCGGGCCCAGCTGCAACTGCACTTGCCCGCCAACCGGTTGCAGGCGG
TGGAGGGAGGGGAAGTGGTGCTTCCAGCGTGGTACACCTTGACGCGGGAGGTGTCTTCATCCC
AGCCATGGGAGGTGCCCTTTGTGATGTGGTTCTTCAAACAGAAAGAAAAGGAGGATCAGGTGT
TGTCTACATCAATGGGGTCACAACAAGCAAACCTGGAGTATCCTTGGTCTACTCCATGCCCT
CCCGGAACCTGTCCCTGCGGCTGGAGGGTCTCCAGGAGAAAGACTCTGGCCCCCTACAGCTGCT
CCGTGAATGTGCAAGACAAACAAGGCAAATCTAGGGGCCACAGCATCAAACCTTAGAACTCA
ATGTACTGGTTCCTCCAGCTCCTCCATCCTGCCGTCTCCAGGGTGTGCCCCATGTGGGGGCAA
ACGTGACCCTGAGCTGCCAGTCTCCAAGGAGTAAGCCCGCTGTCCAATACCAGTGGGATCGGC
AGCTTCCATCCTTCCAGACTTTCTTTGCACCAGCATTAGATGTCATCCGTGGGTCTTTAAGCC
TCACCAACCTTTCGTCTTCCATGGCTGGAGTCTATGTCTGCAAGGCCACAATGAGGTGGGCA
CTGCCCAATGTAATGTGACGCTGGAAGTGAGCACAGGGCCTGGAGCTGCAGTGGTTGCTGGAG
CTGTTGTGGGTACCCTGGTTGGACTGGGGTTGCTGGCTGGGCTGGTCCTCTTGTACCACCGCC
GGGGCAAGGCCCTGGAGGAGCCAGCCAATGATATCAAGGAGGATGCCATTGCTCCCCGGACCC
TGCCCTGGCCCAAGAGCTCAGACACAATCTCCAAGAATGGGACCCTTTCCTCTGTACCTCCG
CACGAGCCCTCCGGCCACCCCATGGCCCTCCCAGGCCTGGTGCATTGACCCCCACGCCAGTC
TCTCCAGCCAGGCCCTGCCCTACCAAGACTGCCACGACAGATGGGGCCACCCCTCAACCAA
TATCCCCCATCCCTGGTGGGGTTTCTTCCCTCTGGCTTGAGCCGCATGGGTGCTGTGCCTGTGA
TGGTGCCTGCCCAGAGTCAAGCTGGCTCTCTGGTAT**TGA**TGACCCCACTCATTTGGCTAAAG
GATTTGGGGTCTCTCCTTCTATAAGGGTCACCTCTAGCACAGAGGCCTGAGTCATGGGAAAG
AGTCACACTCCTGACCCTTAGTACTCTGCCCCACCTCTCTTTACTGTGGGAAAACCATCTCA
GTAAGACCTAAGTGTCCAGGAGACAGAAGGAGAAGAGGAAGTGGATCTGGAATTGGGAGGAGC
CTCCACCCACCCCTGACTCCTCCTTATGAAGCCAGCTGCTGAAATTAGCTACTACCAAGAGT
GAGGGGCAGAGACTTCCAGTCACTGAGTCTCCAGGCCCCCTTGATCTGTACCCACCCCTAT
CTAACACCACCCTTGGCTCCCCTCCAGCTCCCTGTATTGATATAACCTGTCAGGCTGGCTTG
GTTAGGTTTTACTGGGGCAGAGGATAGGGAATCTCTTATTAAACTAACATGAAATATGTGTT
GTTTTCATTTGCAAATTTAAATAAAGATACATAATGTTTGTATGAAAAA

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FIGURE 338

MISLPGPLVTNLLRFLFLGLSALAPPSRAQLQLHLPANRLQAVEGGEVVLPAWYTLHGCVSSS
QPWEVPPFVMWFFKQKEKEDQVLSYINGVTTSKPGVSLVYSMPSRNLSLRLEGLQEKDSGPYSC
SVNVQDKQGKSRGHSIKTLELNVLVPPAPPSCRLQGVPHVGANVTLSQSPRSKPAVQYQWDR
QLPSFQTFEFAPALDVIRGSLSLTNLSSSMAGVYVCKAHNEVGTAQCNVTLEVSTGPGAADVAG
AVVGTLVGLGLLAGLVLLYHRRGKALEEPANDIKEDAIAPRTLWPWKSSDTISKNGTLSSVTS
ARALRPPHGPFRPGALTPTPSLSSQALPSPRLPTTDGAHPQPISPIPGGVSSSSGLSRMGAVPV
MVPAQSQAGSLV

Important features:**Signal peptide:**

amino acids 1-29

Transmembrane domain:

amino acids 245-267

N-glycosylation site.

amino acids 108-112, 169-173, 213-217, 236-240, 307-311

N-myristoylation site.amino acids 90-96, 167-173, 220-226, 231-237, 252-258, 256-262,
262-268, 308-314, 363-369, 364-370**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 164-175

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FIGURE 339

GCAGAACCTTTGCACGCGCACAACTACGGGGACGATTTCTGATTGATTTTTTGGCGCTTTCGATCCACCCTCCT
CCCTTCTC**ATG**GGGACTTTGGGGACAAAGCGTCCCGACCGCCTCGAGCGCTCGAGCAGGGCGCTATCCAGGAGCCA
GGACAGCGTCCGGGAACCAGACCATGGCTCCTGGACCCCAAGATCCTTAAGTTCGTCTCTTCATCGTCGCGGTTTC
TGCTGCCGGTCCGGGTTGACTCTGCCACCATCCCCCGGCAGGACGAAGTTCGCCAGCAGACAGTGGCCCCACAGC
AACAGAGGCGCAGCCTCAAGGAGGAGGAGTGTCCAGCAGGATCTCATAGATCAGAATATACTGGAGCCTGTAACC
CGTGCACAGAGGGTGTGGATTACACCATTGCTTCCAACAATTTGCCTTCTTGCCTGCTATGTACAGTTTGTAAAT
CAGGTCAAAACAAATAAAAGTTCCTGTACCACGACCAGAGACACCGTGTGTGAGTGTGAAAAAGGAAGCTTCCAGG
ATAAAAACTCCCTGAGATGTGCCGGACGTGTAGAACAGGGTGTCCAGAGGGATGGTCAAGGTGAGTAATTGTA
CGCCCCGGAGTGACATCAAGTGCAAAAATGAATCAGCTGCCAGTTCCTACTGGGAAAACCCACAGCAGCGGAGGAGA
CAGTGACCACCATCCTGGGGATGCTTGCCTCTCCCTATCACTACCTTATCATCATAGTGGTTTTAGTCATCATTT
TAGCTGTGGTTGTGGTTGGCTTTTTCATGTCCGAAGAAATTCATTTCTTACCTCAAAGGCATCTGCTCAGGTGGTG
GAGGAGGTCCCGAACGTGTGCACAGAGTCTTTTCCGGCGGCGTTCATGTCTTCACGAGTTCTTGGGGCGGAGG
ACAATGCCCGCAACGAGACCCCTGAGTAACAGATACTTGCAGCCACCCAGGTCTCTGAGCAGGAAATCCAAGGTC
AGGAGCTGGCAGAGCTAACAGGTGTGACTGTAGAGTCGCCAGAGGAGCCACAGCGTCTGCTGGAACAGGCAGAAG
CTGAAGGGTGTCTAGAGGAGGAGGCTGCTGGTTCCAGTGAATGACGCTGACTCCGCTGACATCAGCACCCTTGCTGG
ATGCTTCGGCAACACTGGAAGAAGGACATGCAAGGAAACAATTCAGGACCAACTGGTGGGCTCCGAAAAGCTCT
TTTATGAAGAAGATGAGGCAGGCTCTGCTACGTCTGCTCTG**TGA**AAGAATCTCTTCAGGAAACCAGAGCTTCCCT
CATTTACCTTTTCTCTACAAAGGGAAGCAGCCTGGAAGAAACAGTCCAGTACTTGACCCATGCCCAACAACT
CTACTATCCAATATGGGGCAGCTTACCAATGGTCTTAGAACTTTGTAAACGCACTTGAGTAATTTTTATGAAAT
ACTGCGTGTGATAAGCAAACGGGAGAAATTTATATCAGATTCTTGGCTGCATAGTTATACGATTGTGTATTAAGG
GTGCTTTTAGGCCATGCGGTGGCTCATGCCTGTAATCCCAGCACTTTGATAGGCTGAGGCAGGTGGATTGCTT
GAGCTCGGGAGTTTGAGACCAGCCTCATCAACACAGTGAAACTCCATCTCAATTTAAAAAGAAAAAAGTGGTTT
TAGGATGTCAATCTTTGCAGTCTTTCATCATGAGACAAGTCTTTTTTTCTGCTTCTTATATTGCAAGCTCCATCT
CTACTGGTGTGTGCATTTAATGACATCTAACTACAGATGCCGCACAGCCACAATGCTTTGCCTTATAGTTTTTTTA
ACTTTAGAACGGGATTATCTTGTATTACCTGTATTTTCAGTTTCGGATATTTTTGACTTAATGATGAGATTATC
AAGACGTAGCCCTATGCTAAGTCATGAGCATATGACTTACGAGGGTTCGACTTAGAGTTTTGAGCTTTAAGATA
GGATTATTGGGGCTTACCCCCACCTTAATTAGAGAAACATTTATATTGCTTACTACTGTAGGCTGTACATCTCTT
TTCCGATTTTTGTATAATGATGTAACATGGA AAAA ACTTTAGGAAATGCACTTATTAGGCTGTTTACATGGGTTG
CCTGGATACAAATCAGCAGTCAAAAATGACTAAAAATATACTAGTGACGGAGGGAGAAATCCTCCCTCTGTGGG
AGGCACTTACTGCATTCAGTTCTCCCTCCTGCGCCCTGAGACTGGACCAGGGTTTGATGGCTGGCAGCTTCTCA
AGGGGCAGCTTGTCTTACTTGTTAATTTTAGAGGTATATAGCCATATTTATTTATAAATAAATATTTATTTATTT
ATTTATAAGTAGATGTTTACATATGCCCAGGATTTTGAAGAGCCTGGTATCTTTGGGAAGCCATGTGTCTGGTTT
GTCGTGCTGGGACAGTCATGGGACTGCATCTTCCGACTTGTCCACAGCAGATGAGGACAGTGAGAATTAAGTTAG
ATCCGAGACTGCGAAGAGCTTCTCTTTCAAGCGCCATTACAGTTGAACGTTAGTGAATCTTGAGCCTCATTTGGG
CTCAGGGCAGAGCAGGTGTTTATCTGCCCCGGCATCTGCCATGGCATCAAGAGGGAAGAGTGGACGGTGTCTGGG
AATGGTGTGAAATGGTTGCCGACTCAGGCATGGATGGGCCCCCTCTCGCTTCTGGTGGTCTGTGAACTGAGTCCCT
GGGATGCCTTTTAGGGCAGAGATTCCTGAGCTGCGTTTTAGGGTACAGATTCCTGTGTTGAGGAGCTTGGCCCCCT
CTGTAAGCATCTGACTCATCTCAGAGATATCAATCTTAAACACTGTGACAACGGGATCTAAAAATGGCTGACACA
TTTGCTCTGTGTACGTTCCATTATTTTATTTAAAAACCTCAGTAATCGTTTTAGCTTCTTTCCAGCAAACTCT
TCTCCACAGTAGCCCAAGTCTGTTGGTAGGATAAATTACGGATATAGTCATTCTAGGGGTTTCAGTCTTTTCCATCTC
AAGGCATTGTGTGTTTTGTTCCGGGACTGGTTTGGCTGGGACAAAGTTAGAACTGCCTGAAGTTTCGCACATTTCAG
ATTGTTGTGTCCATGGAGTTTTTAGGAGGGGATGGCCTTTCCGGTCTTCGCACTTCCATCCTCTCCCACTTCCATC
TGGCGTCCCACACCTTGTCCCCTGCACTTCTGGATGACACAGGGTGTGCTGCCTCCTAGTCTTTGCCTTTGCTG
GGCCTTCTGTGCAGGAGACTTGGTCTCAAAGCTCAGAGAGAGCCAGTCCGGTCCCAGCTCCTTTGTCCCTTCTC
AGAGGCCTTCTTGAAGATGCATCTAGACTACCAGCCTTATCAGTGTTTAAGCTTATTCCTTTAACATAAGCTTC
CTGACAACATGAAATTTGTTGGGGTTTTTTGGCGTTGGTTGATTGTTTGGTTTTATACCCGGGCCAAAT
AGCACATAACACCTGGTTATATATGAAATACTCATATGTTTATGACCAAAATAAATATGAAACCTCATRTTAAAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAA

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FIGURE 340

MGLWGQSVPTASSARAGRYPGARTASGTRPWLLDPKILKFVVFIVAVLLPVRVDSATIPRQDEVPPQQTVA PQQR
RSLKEEECPAGSHRSEYTGACNPCTEGVDYTIASNNLPSCLLCTVCKSGQTNKSSCTTTTRDTVCQCEKGSFQDN
SPEMCRTCRTGCPRGMVKVSNCTPRSDIKCKNESAASSTGKTPAAEETVTTILGMLASPYHYLIIIVVLVILAV
VVVGFSCRKKFISYLGKICSGGGGGPERVHRVLFRRRSCPSRVPGAEDNARNETLSNRYLQPTQVSEQEIQQQEL
AELTGVTVESPEEPQRLLEQAEAGCQRRRLVLPVNDADSADISTLLDASATLEEGHAKETIQDQLVGSEKLFYE
EDEAGSATSCSCL

Important features:**Transmembrane domains:**

amino acids 35-52, 208-230

N-glycosylation sites.

amino acids 127-131, 182-186, 277-281

Glycosaminoglycan attachment site.

amino acids 245-249

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 260-264

N-myristoylation sites.

amino acids 21-27, 86-92, 102-108, 161-167, 242-248, 270-276, 297-303, 380-386

ATP/GTP-binding site motif A (P-loop).

amino acids 185-193

TNFR/NGFR cysteine-rich region.

amino acids 99-139

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FIGURE 341

GCCTCTGAATTGTTGGGCAGTCTGGCAGTGGAGCTCTCCCCGGTCTGACAGCCACTCCAGAGG
CCATGCTTCGTTTCTTGCCAGATTTGGCTTTCAGCTTCCTGTTAATTCTGGCTTTGGGCCAGG
CAGTCCAATTTCAAGAATATGTCTTTCTCCAATTTCTGGGCTTAGATAAGGCGCCTTCACCCC
AGAAGTTCCAACCTGTGCCTTATATCTTGAAGAAAATTTTCCAGGATCGCGAGGCAGCAGCGA
CCACTGGGGTCTCCCGAGACTTATGCTACGTAAAGGAGCTGGGCGTCCGCGGGAATGTA CTTC
GCTTTCTCCCAGACCAAGGTTTCTTTCTTTACCCAAAGAAAATTTCCCAAGCTTCCTCCTGCC
TGCAGAAAGCTCCTCTACTTTAACCCTGTCTGCCATCAAAGAAAGGGAACAGTTGACATTGGCCC
AGCTGGGCCTGGACTTGGGGCCCAATTCTTACTATAACCTGGGACCAGAGCTGGA ACTGGCTC
TGTTCCCTGGTTCAGGAGCCTCATGTGTGGGGCCAGACCACCCCTAAGCCAGGTAAAATGTTTG
TGTTGCGGTCAGTCCCATGGCCACAAGGTGCTGTTCACTTCAACCTGCTGGATGTAGCTAAGG
ATTGGAATGACAACCCCCGGAAAAATTTTCGGGTATTTCCTGGAGATACTGGTCAAAGAAGATA
GAGACTCAGGGGTGAATTTTCAGCCTGAAGACACCTGTGCCAGACTAAGATGCTCCCTTCATG
CTTCCCTGCTGGTGGTGA CTCTCAACCCTGATCAGTGCCACCCTTCTCGGAAAAGGAGAGCAG
CCATCCCTGTCCCCAAGCTTTCTTGTAAGAACCTCTGCCACCGTCACCAGCTATTCATTA ACT
TCCGGGACCTGGGTTGGCACAAGTGGATCATTGCCCCCAAGGGGTTCATGGCAAATTACTGCC
ATGGAGAGTGTCCTTCTCACTGACCATCTCTCTCAACAGCTCCAATTATGCTTTCATGCAAG
CCCTGATGCATGCCGTTGACCCAGAGATCCCCCAGGCTGTGTGTATCCCCACCAAGCTGTCTC
CCATTTCCATGCTCTACCAGGACAATAATGACAATGTCATTCTACGACATTATGAAGACATGG
TAGTCGATGAATGTGGGTGTGGGTAGGATGTCAGAAATGGGAATAGAAGGAGTGTTCTTAGGG
TAAATCTTTTAATAAAACTACCTATCTGGTTTATGACCACTTAGATCGAAATGTC

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FIGURE 342

MLRFLPDLAFSFLILALGQAVQFQEYVFLQFLGLDKAPSPQKFQPVYPYILKKIFQDREAAAT
TGVSRDLICYVKELGVRGNVLRFLPDQGFFLYPKKISQASSCLQKLLYFNLSAIKEREQLTLAQ
LGLDLGPNSYYNLGPELELALFLVQEPHVWGQTPKPGKMFVLRVSPWPQGAVHFNLLDVAKD
WNDNPRKNFGLFLEILVKEDRDSGVNFQPEDTCARLRCSLHASLLVVTLNPDQCHPSRKRRAA
IPVPKLSCKNLCHRHQLFINFRDLGWHKWIIAPKGFMANYPCHGECPFSLTISLNSSNYAFMQA
LMHAVDPEIPQAVCIPTKLSPISMLYQDNNDNVILRHYEDMVVDECGCG

Important features:**Signal peptide:**

amino acids 1-21

N-glycosylation sites.

amino acids 112-116, 306-310

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 96-100

N-myristoylation site.

amino acids 77-83

TGF-beta family proteins.

amino acids 264-299, 327-341, 345-364

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FIGURE 343

CCCACGCGTCCGGCCTTCTCTCTGGACTTTGCATTTCCATTCCTTTTCATTGACAACTGACTTTTTTTATTTCT
TTTTTTCCATCTCTGGGCCAGCTTGGGATCCTAGGCCGCCCTGGGAAGACATTTGTGTTTTACACACATAAGGAT
CTGTGTTTTGGGGTTTTCTTCTCCTCCCCTGACATTGGCATTGCTTAGTGGTTGTGTGGGGAGGGAGACCACGTGG
GCTCAGTGCTTGCTTGCACCTTATCTGCCTAGGTACATCGAAGTCTTTTGACCTCCATACAGTGATTATGCCTGTC
ATCGCTGGTGGTATCCTGGCGGCCCTTGCTCCTGCTGATAGTTGTCTGCTCTGTCTTTACTTCAAAAATACACAAC
GCGCTAAAAGCTGCAAAGGAACCTGAAGCTGTGGCTGTAAAAAATCACAACCCAGACAAGGTGTGGTGGGCCAAG
AACAGCCAGGCCAAAACCATTTGCCACGGAGTCTTGTCTGCCCCTGCAGTGCTGTGAAGGATATAGAATGTGTGCC
AGTTTTTGATTCCCTGCCACCTTGCTGTTGCGACATAAATGAGGGCCCTCTGAGTTAGGAAAGGCTCCCTTCTCAAA
GCAGAGCCCTGAAGACTTCAATGATGTCAATGAGGCCACCTGTTTGTGATGTGCAGGCACAGAAGAAAGGCACAG
CTCCCCATCAGTTTCAATGGAAAATAACTCAGTGCCTGCTGGGAACCAGCTGCTGGAGATCCCTACAGAGAGCTTC
CACTGGGGGGCAACCTTCCAGGAAGGAGTTGGGGAGAGAGAACCCTCACTGTGGGGAATGCTGATAAACCAGTCA
CACAGCTGCTCTATTCTCACACAAATCTACCCCTTGCGTGGCTGGAACCTGACGTTTCCCTGGAGGTGTCCAGAAA
GCTGATGTAACACAGAGCCTATAAAAGCTGTGGTCTCTTAAGGCTGCCAGCGCCTTGCCAAAATGGAGCTTGTA
AGAAGGCTCATGCCATTGACCCTCTTAATTTCTCTCCTGTTTGGCGGAGCTGACAATGGCGGAGGCTGAAGGCAAT
GCAAGCTGCACAGTCAGTCTAGGGGGTGCCAATATGGCAGAGACCCACAAAGCCATGATCTGCAACTCAATCCC
AGTGAGAAGTGCACCTGGACAATAGAAAGACCAGAAAACAAAAGCATCAGAATTATCTTTTCTATGTCCAGCTT
GATCCAGATGGAAGCTGTGAAAGTGAAAACATTAAAGTCTTTGACGGAACCTCCAGCAATGGGCCTCTGCTAGGG
CAAGTCTGCAGTAAAAACGACTATGTTCTGTATTTGAATCATCATCCAGTACATTGACGTTTCAAATAGTTACT
GACTCAGCAAGAATTCAAAGAAGTGTCTTTGTCTTCTACTACTTCTTCTCTCTAACATCTCTATTCCAAACTGT
GGCGGTTACCTGGATACCTTGAAGGATCCTTACCAGCCCCAATTACCCAAAGCCGCATCCTGAGCTGGCTTAT
TGTGTGTGGCACATACAAGTGGAGAAAGATTACAAGATAAAACTAAACTTCAAAGAGATTTTCTAGAAAATAGAC
AAACAGTGCAAATTTGATTTTCTTGCCATCTATGATGGCCCTCCACCAACTCTGGCCTGATTGGACAAGTCTGT
GGCCGTGTGACTCCCACCTTCGAATCGTCATCAAACCTCTGACTGTCGTGTTGTCTACAGATTATGCCAATTCT
TACCGGGGATTTTCTGCTTCTTACACCTCAATTTATGCAGAAAACATCAACACTACATCTTTAACTTGCTCTTCT
GACAGGATGAGAGTTATTATAAGCAAATCCTACCTAGAGGCTTTTAACTCTAATGGGAATAACTTGCAACTAAAA
GACCCAACTTGCAGACCAAAATTATCAAATGTTGTGGAATTTTCTGTCCCTCTTAATGGATGTGGTACAATCAGA
AAGGTAGAAGATCAGTCAATTACTTACACCAATATAATCACCTTTTCTGCATCCTCAACTTCTGAAGTGATCACC
CGTCAGAAACAACCTCCAGATTATTGTGAAGTGTGAAATGGGACATAATTCTACAGTGGAGATAATATACATAACA
GAAGATGATGTAATACAAAGTCAAAATGCACTGGGCAAATATAACACCAGCATGGCTCTTTTTGAATCCAATTCA
TTTGAAAAGACTATACTTGAATCACCATATTATGTGGATTTGAACCAAACCTTTTTTGTTCAGTTAGTCTGCAC
ACCTCAGATCCAAATTTGGTGGTGTCTTGATACCTGTAGAGCCTCTCCCACCTCTGACTTTGCATCTCCAACC
TACGACCTAATCAAGAGTGGATGTAGTCGAGATGAAACTTGTAAGGTGTATCCCTTATTTGGACACTATGGGAGA
TTCCAGTTTAAATGCCTTTAAATTCTTGAGAAGTATGAGCTCTGTGTATCTGCAGTGTAAAGTTTTGATATGTGAT
AGCAGTGACCACAGTCTCGCTGCAATCAAGGTTGTGTCTCCAGAAGCAAACGAGACATTTCTTCATATAAATGG
AAAACAGATTCCATCATAGGACCCATTTCGTCTGAAAAGGGATCGAAGTGCAAGTGGCAATTCAGGATTTTCAGCAT
GAAACACATGCGGAAGAAAACCTCAAACCAGCCTTTCAACAGTGTGCATCTGTTTTCTTCATGGTTCTAGCTCTG
AATGTGGTGAATGTAGCGACAATCACAGTGAGGCATTTTGTAAATCAACGGGCAGACTACAAATACCAGAAGCTG
CAGAAGTATTAACCTAACAGGTCCAACCCTAAGTGAGACATGTTTCTCCAGGATGCCAAAGGAAATGCTACCTCGT
GGCTACACATATTATGAATAAATGAGGAAGGGCCTGAAAGTGACACACAGGCCTGCATGTAAAAAA

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FIGURE 344

MELVRRRLMPLTLLILSCLAELTMAEAEGNASCTVSLGGANMAETHKAMILQLNPSENCTWTIE
RPENKSIRIIIFSIVQLDPDGSCSENIKVFDGTSSNGPLLQVCSKNDYVPVFESSSSTLTFO
IVTDSARIQRTVFVFFYYFFSPNISIPNCGGYLDTLEGSFTSPNYPKPHPELAYCVWHIQVEKD
YKIKLNFKEIFLEIDKQCKFDFLAIYDGPSTNSGLIGQVCGRVTPTFESSSNSLTVVVLDYD
NSYRGFSASYTSIYAENINTTSLTCSSDRMRVVIISKSYLEAFNSNGNNLQLKDPTCRPKLSNV
VEFSVPLNGCGTIRKVEDQSITYTNIITFSASSTSEVITRQQLQIIVKCEMGHNSTVEIIYI
TEDDVIQSQNALGKYNTSMALFESNSFEKTILESPYYVDLNQTLFVQVSLHTSDPNLVVFLDT
CRASPTSDFASPTYDLIKSGCSRDETCKVYPLFGHYGRFQFNAFKFLRSMSSVYLQCKVLICD
SSDHQSRCNQGCVSRSKRDISSYKWKTDSSIIGPIRLKRDRSASGNSGFQHETHAEETPNQPFN
SVHLFSFMVLALNVVTVATITVRHFVNQRADYKYQKLQNY

Important features:**Signal sequence:**

amino acids 1-24

Transmembrane domain:

amino acids 571-586

N-glycosylation site.amino acids 29-33, 57-61, 67-71, 148-152, 271-275, 370-374,
394-398, 419-423**Casein kinase II phosphorylation site.**amino acids 22-26, 108-112, 289-293, 348-352, 371-375, 379-383,
408-412, 463-467, 520-524, 556-560**Tyrosine kinase phosphorylation site.**

amino acids 172-180, 407-415, 407-416, 519-528

N-myristoylation site.

amino acids 28-34, 38-44, 83-89, 95-101, 104-110, 226-232

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 7-18

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FIGURE 345

TGGGGGCCCCCAGGCTCGCGCGTGGAGCGAAGCAGC**ATG**GGGCAGTCGGTGCGCGCTGGCCCTGGCGGTGCTCTC
GGCCTTGCTGTGTCAAGTCTGGAGCTCTGGGGTGTTCGAAGCTGAAGCTGCAGGAGTTTCGTCACAAAGAAGGGGCT
GCTGGGGAAACCGCAATTGCTGCCGCGGGGGCGCGGGGGCCACCGCCGTGCGCCTGCCGGACCTTCTTCCGCGTGTG
CCTCAAGCACTACCAGGCCAGCGTGTCCCCGAGCCGCCCTGCACCTACGGCAGCGCCGTACCCCCGTGCTGGG
CGTCGACTCCTTCAGTCTGCCCCGACGGCGGGGGCGCCGACTCCGCGTTTCAGCAACCCCATCCGCTTCCCCTTCGG
CTTCACCTGGCCGGGCACCTTCTCTCTGATTATTGAAGCTCTCCACACAGATTCTCCTGATGACCTCGCAACAGA
AAACCCAGAAAAGACTCATCAGCCGCTGGCCACCCAGAGGCACCTGACGGTGGGCGAGGAGTGGTCCCAGGACCT
GCACAGCAGCGGCCGCACGGACCTCAAGTACTCCTACCGCTTCGTGTGTGACGAACACTACTACGGAGAGGGCTG
CTCCGTTTTCTGCCGTCCCCGGGACGATGCCTTCGGCCACTTCACCTGTGGGGAGCGTGGGGAGAAAGTGTGCAA
CCCTGGCTGGAAAGGGCCCTACTGCACAGAGCCGATCTGCCTGCCTGGATGTGATGAGCAGCATGGATTTTGTGA
CAAACCAGGGGAATGCAAGTGCAGAGTGGGCTGGCAGGGCCGGTACTGTGACGAGTGTATCCGCTATCCAGGCTG
TCTCCATGGCACCTGCCAGCAGCCCTGGCAGTGCAACTGCCAGGAAGGCTGGGGGGGCTTTTCTGCAACCAGGA
CCTGAAGTACTGCACACACCATAAGCCCTGCAAGAATGGAGCCACCTGCACCAACACGGGCCAGGGGAGCTACAC
TTGCTCTTGCCGGCTGGGTACACAGGTGCCACCTGCGAGCTGGGGATTGACGAGTGTGACCCAGCCCTTGTA
GAACGGAGGGAGCTGCACGGATCTCGAGAACAGTACTCCTGTACCTGCCACCCGGCTTCTACGGCAAAATCTG
TGAATTGAGTGCCATGACCTGTGCGGACGGCCCTTGCTTTAACGGGGTTCGGTGTCTCAGACAGCCCCGATGGAGG
GTACAGCTGCCGCTGCCCGTGGGCTACTCCGGCTTCAACTGTGAGAAGAAAATTGACTACTGCAGCTCTTCACC
CTGTTCTAATGGTGCCAAGTGTGTGGACCTCGGTGATGCCTACCTGTGCCGCTGCCAGGCCGGCTTCTCGGGGAG
GCACTGTGACGACAACGTGGACGACTGCGCCTCCTCCCCGTGCGCCAACGGGGGCACCTGCCGGGATGGCGTGAA
CGACTTCTCCTGCACCTGCCCCGCTGGCTACACGGGCAGGAAGTGCAGTGCCCCCGTCAGCAGGTGCGAGCACGC
ACCTGCCACAATGGGGCCACCTGCCACGAGAGGGGGCCACCGCTATGTGTGCGAGTGTGCCCGAGGCTACGGGGG
TCCCAACTGCCAGTTCTCTGCTCCCCGAGCTGCCCCCGGGGCCAGCGGTGGTGGACCTCACTGAGAAGCTAGAGGG
CCAGGGCGGGCCATTCCCCCTGGGTGGCCGTGTGCGCCGGGGTCATCCTTGTCTCATGCTGCTGCTGGGCTGTGC
CGCTGTGGTGGTCTGCGTCCGGCTGAGGCTGCAGAAGCACCGGCCCCAGCCGACCCCTGCCGGGGGGAGACGGA
GACCATGAACAACCTGGCCAACCTGCCAGCGTGAGAAGGACATCTCAGTCAGCATCATCGGGGCCACGCAGATCAA
GAACACCAACAAGAAGGCGGACTTCCACGGGGACCACAGCGCCGACAAGAATGGCTTCAAGGCCCGCTACCCAGC
GGTGGACTATAACCTCGTGCAGGACCTCAAGGGTGACGACACCGCCGTCAGGGACGCGCACAGCAAGCGTGACAC
CAAGTGCCAGCCCCAGGGCTCCTCAGGGGAGGAGAAGGGGACCCCGACCACACTCAGGGGTGGAGAAGCATCTGA
AAGAAAAAGGCCGACTCGGGCTGTTCAACTTCAAAAGACACCAAGTACCAGTCGGTGTACGTCATATCCGAGGA
GAAGGATGAGTGCGTCATAGCAACTGAGGTG**TAAA**ATGGAAGTGAGATGGCAAGACTCCCGTTTCTCTTAAATA
AGTAAATTTCCAAGGATATATGCCCAACGAATGCTGCTGAAGAGGAGGGAGGCCTCGTGGACTGCTGCTGAGAA
ACCGAGTTCAGACCGAGCAGGTTCTCCTCCTGAGGTCTCGACGCTGCCGACAGCCTGTGCGGGCCCGGCCCC
TGCGGCACTGCCTTCCGTGACGTGCGCGTTGCACTATGGACAGTTGCTCTTAAGAGAATATATATTTAAATGGGT
GAACTGAATTACGCATAAGAAGCATGCACTGCCTGAGTGTATATTTTGGATTCTTATGAGCCAGTCTTTTCTTGA
ATTAGAAACACAAACACTGCCTTTATTGTCCTTTTTGATACGAAGATGTGCTTTTTCTAGATGGAAAAGATGTGT
GTTATTTTTTGGATTGTAAAAATATTTTTTCATGATATCTGTAAAGCTTGAGTATTTTGTGATGTTTCGTTTTTTA
TAATTTAAATTTTGGTAAATATGTACAAAGGCACTTCGGGTCTATGTGACTATATTTTTTTGTATATAAATGTAT
TTATGGAATATTGTGCAATGTTATTTGAGTTTTTTACTGTTTTGTTAATGAAGAAATTCCTTTTTTAAATATTT
TTCCAAAATAAATTTTATGAATGACAAAAA

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FIGURE 346

MGSRCALALAVLSALLCQVWSSGVFELKLQEFVNKKGLLGNRNCCRGGAGPPPCACRTFFRVC
LKHYQASVSPEPPCTYGSAVTPVLGVDSFSLPDGGGADSAFSNPIRFPFGFTWPGTFSLIIEA
LHTDSPDDLATENPERLISRLATQQRHLTVGEEWSQDLHSSGRITDLKYSYRFVCDEHYYGEGCS
VFCRPRDDAFGHFTCGERGEKVCNPGWKGPYCTEPICLPGCDEQHGFCDKPGECKCRVWQGR
YCDECIRYPGCLHGTCQQPWQCNCQEGWGGLFCNQDLNYCTHHKPCKNATCTNTGQGSYTCS
CRPGYTGATCELGIDECDPSPCKNGGSCTDLENSYSCTCPPGFYKGICELSAMTCADGPCFNG
GRCSDSPDGGYSCRCVPVGYSGFNCEKKIDYCSSSPCSNGAKCVDLGDAYLCRCQAGFSGRHCD
DNVDDCASSPCANGGTCTRDGVNDFSCCTCPPGYTGRNCSAPVSRCEHAPCHNGATCHERGHRYV
CECARGYGGPNCQFLLPELPPGPAVVDLTKLEGQGGPFPWVAVCAGVILVLMMLLLGCAAVVV
CVRLRLQKHRPPADPCRGETETMNNLANCQREKDISVSIIGATQIKNTNKKADFHGDHSADKN
GFKARYPAVDYNLVQDLKGDDTAVRDAHSKRDTKCQPQGSSEEEKGTPTTLRGGEASERKRPD
SGCSTSKDTKYQSVYVISEEKDECVIATEV

Important features:**Signal sequence:**

Amino acids 1-21

Transmembrane domain:

Amino acids 546-566

N-glycosylation site:

Amino acids 477-481

cAMP- and cGMP-dependent protein kinase phosphorylation site:

Amino acids 660-664

Tyrosine kinase phosphorylation sites:

Amino acids 176-185;252-261

N-myristoylation sites:Amino acids 2-8;37-43;40-46;98-104;99-105;262-268;281-287;
282-288;301-307;310-316;328-334;340-344;378-384;387-393;512-518;
676-682;683-689;695-701**Aspartic acid and asparagine hydroxylation sites:**

Amino acids 343-355;420-432;458-470

Prokaryotic membrane lipoprotein lipid attachment site:

Amino acids 552-563

EGF-like domain cysteine pattern signature:Amino acids 243-255;274-286;314-326;352-364;391-403;429-441;
467-479;505-517

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FIGURE 347

CCCACGCGTCCGCACCTCGGCCCCGGGCTCCGAAGCGGCTCGGGGGCGCCCTTTCGGTCAACA
TCGTAGTCCACCCCCTCCCCATCCCCAGCCCCGGGGATTTCAGGCTCGCCAGCGCCCAGCCAG
GGAGCCGGCCGGGAAGCGCGATGGGGGCCCCAGCCGCCTCGCTCCTGCTCCTGCTCCTGCTGT
TCGCCTGCTGCTGGGCGCCCGGCGGGGCCAACCTCTCCAGGACGACAGCCAGCCCTGGACAT
CTGATGAAACAGTGGTGGCTGGTGGCACCGTGGTGCTCAAGTGCCAAGTGAAAGATCACGAGG
ACTCATCCCTGCAATGGTCTAACCTGCTCAGCAGACTCTCTACTTTGGGGAGAAGAGAGCCC
TTCGAGATAATCGAATTCAGCTGGTTACCTCTACGCCCCACGAGCTCAGCATCAGCATCAGCA
ATGTGGCCCTGGCAGACGAGGGCGAGTACACCTGCTCAATCTTCACTATGCCTGTGCGAACTG
CCAAGTCCCTCGTCACTGTGCTAGGAATTCCACAGAAGCCCATCATCACTGGTTATAAATCTT
CATTACGGGAAAAAGACACAGCCACCCTAAACTGTCAGTCTTCTGGGAGCAAGCCTGCAGCCC
GGCTCACCTGGAGAAAGGGTGACCAAGAACTCCACGGAGAACCAACCCGCATACAGGAAGATC
CCAATGGTAAAACCTTCACTGTCAGCAGCTCGGTGACATTCCAGGTACCCGGGAGGATGATG
GGGCGAGCATCGTGTGCTCTGTGAACCATGAATCTCTAAAGGGAGCTGACAGATCCACCTCTC
AACGCATTGAAGTTTTATACACACCAACTGCGATGATTAGGCCAGACCCTCCCCATCCTCGTG
AGGGCCAGAAGCTGTTGCTACACTGTGAGGGTCGCGGCAATCCAGTCCCCCAGCAGTACCTAT
GGGAGAAGGAGGGCAGTGTGCCACCCCTGAAGATGACCCAGGAGAGTGCCCTGATCTTCCCTT
TCCTCAACAAGAGTGACAGTGGCACCTACGGCTGCACAGCCACCAGCAACATGGGGCAGCTACA
AGGCCTACTACACCCTCAATGTTAATGACCCCAGTCCGGTGCCCTCCTCCTCCAGCACCTACC
ACGCCATCATCGGTGGGATCGTGGCTTTCATTGTCTTCCTGCTGCTCATCATGCTCATCTTCC
TTGGCCACTACTTGATCCGGCACAAAGGAACCTACCTGACACATGAGGCAAAAGGCTCCGACG
ATGCTCCAGACGCGGACACGGCCATCATCAATGCAGAAGGCGGGCAGTCAGGAGGGGACGACA
AGAAGGAATATTTTCATCTAGAGGCGCCTGCCCCACTTCCTGCGCCCCCAGGGGCCCTGTGGGG
ACTGCTGGGGCCGTCACCAACCCGGACTTGTACAGAGCAACCGCAGGGCCGCCCTCCCGCTT
GCTCCCCAGCCCACCCACCCCCCTGTACAGAATGTCTGCTTTGGGTGCGGTTTTGTACTCGGT
TTGGAATGGGGAGGGAGGAGGGCGGGGGGAGGGGAGGGTTGCCCTCAGCCCTTTCGGTGGCTT
CTCTGCATTTGGGTTATTATTATTTTTGTAAACAATCCCAAATCAAATCTGTCTCCAGGCTGGA
GAGGCAGGAGCCCTGGGGTGAGAAAAGCAAAAAACAAACAAAAACA

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FIGURE 348

MGAPAASLLLLLLLLFACCWAPGGANLSQDDSQPWTSDETVVAGGTVVLKCQVKDHEDSSLQWS
NPAQQTLYFGEKRALRDNRIQLVTSTPHELSSISINVALADEGEYTCSI FTMPVRTAKSLVTV
LGIPQKPIITGYKSSLREKDTATLNCQSSGSKPAARLTWRKGDQELHGEPTRIQEDPNGKTFT
VSSSVTFQV TREDDGASIVCSVNHESLKGADRSTSQRIEVLYTPTAMIRPDPPHPREGQKLLL
HCEGRGNPVPQQYLWEKEGSPPLKMTQESALIFPFLNKSDSGTYGCTATSNMGSYKAYYTLN
VNDPSPVPSSSSTYHAIIGGIVAFIVFLLIMLI FLGHYLRHKGTYLTHEAKGSDDAPDADT
AIINAEGGQSGGDDKKEYFI

Important features:**Signal sequence:**

amino acids 1-20

Transmembrane domain:

amino acids 331-352

N-glycosylation site.

amino acids 25-29, 290-294

Casein kinase II phosphorylation site.

amino acids 27-31, 35-39, 89-93, 141-145, 199-203, 388-392

N-myristoylation site.amino acids 2-8, 23-29, 156-162, 218-224, 295-301, 298-304,
306-310, 334-340, 360-364, 385-389, 386-390**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 7-18

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FIGURE 349

ACTTGCCATCACCTGTTGCCAGTGTGGAAAAATTCTCCCTGTTGAATTTTTTGCACATGGAGGACAGCAGCAAAG
AGGGCAACACAGGCTGATAAGACCAGAGACAGCAGGGAGATTATTTTACCATACGCCCTCAGGACGTTCCCTCTA
GCTGGAGTTCTGGACTTCAACAGAACCCCATCCAGTCATTTTGATTTTGCTGTTTATTTTTTTTTTCTTTTTCTT
TTTCCCACCACATTGTATTTTATTTCCGTACTTCAGAAATGGGCCTACAGACCACAAAGTGGCCCAGCCATGGGG
CTTTTTTCTGAACTCTGGCTTATCATTTCCCTGGGGCTCTACTCACAGGTGTCCAAACTCCTGGCCTGCCCTA
GTGTGTGCCGCTGCGACAGGAACCTTTGTCTACTGTAATGAGCGAAGCTTGACCTCAGTGCCCTCTTGGGATCCCGG
AGGGCGTAACCGTACTCTACCTCCACAACAACCAATTAATAATGCTGGATTTCCTGCAGAACTGCACAATGTAC
AGTCGGTGCACACGGTCTACCTGTATGGCAACCAACTGGACGAATTCCCATGAACCTTCCCAAGAATGTCAGAG
TTCTCCATTTGCAGGAAAACAATATTCAGACCATTTACGGGGCTGCTCTTGCCAGCTCTTGAAGCTTGAAGAGC
TGCACCTGGATGACAACCTCCATATCCACAGTGGGGGTGGAAGACGGGGCCTTCCGGGAGGCTATTAGCCTCAAAT
TGTTGTTTTTGTCTAAGAATCACCTGAGCAGTGTGCCTGTTGGGCTTCTGTGGACTTGCAAGAGCTGAGAGTGG
ATGAAAATCGAATTGCTGTCATATCCGACATGGCCTTCCAGAATCTCACGAGCTTGGAGCGTCTTATTGTGGACG
GGAACCTCCTGACCAACAAGGTATCGCCGAGGGCACCTTCAGCCATCTCACCAAGCTCAAGGAATTTTCAATTG
TACGTAATTGCTGTCCCACCCTCCTCCCGATCTCCAGGTACGCATCTGATCAGGCTCTATTTGCAGGACAACC
AGATAAACACATTCCTTTGACAGCCTTCTCAAATCTGCGTAAGCTGGAACGGCTGGATATATCCAACAACCAAC
TGCGGATGCTGACTCAAGGGGTTTTTGATAATCTCTCCAACCTGAAGCAGCTCACTGCTCGGAATAACCCTTGGT
TTTGTGACTGCAGTATTAAATGGGTACAGAATGGCTCAAATATATCCCTTCATCTCTCAACGTGCGGGGTTTCA
TGTGCCAAGGTCTGAACAAGTCCGGGGGATGGCCGTGAGGAATTAAATATGAATCTTTTGTCTGTCCCACCA
CGACCCCCGGCCTGCCTCTCTTACCCCCAGCCCCAAGTACAGCTTCTCCGACCACTCAGCCTCCCACCCTCTCTA
TTCCAAACCCTAGCAGAAGCTACACGCCTCCAACCTCCTACCACATCGAAACTTCCCACGATTCTGACTGGGATG
GCAGAGAAAGAGTGACCCACCTATTTCTGAACGGATCCAGCTCTCTATCCATTTTGTGAATGATACTTCCATTC
AAGTCAGCTGGCTCTCTCTCTTACCCTGATGGCATACAAACCTCACATGGGTGAAAATGGGGCCACAGTTTAGTAG
GGGGCATCGTTCAGGAGCGCATAGTCAGCGGTGAGAAGCAACACCTGAGCCTGGTTAACTTAGAGCCCCGATCCA
CCTATCGGATTTGTTTAGTGCCACTGGATGCTTTTAACTACCGCGCGGTAGAAGACACCATTTGTTTCAGAGGCCA
CCACCCATGCCTCCTATCTGAACAACGGCAGCAACACAGCGTCCAGCCATGAGCAGACGACGTCCCACAGCATGG
GCTCCCCCTTTCTGCTGGCGGGCTTGATCGGGGGCGCGGTGATATTTGTGCTGGTGGTCTTGCTCAGCGTCTTTT
GCTGGCATATGCACAAAAAGGGGCGCTACACCTCCCAGAAGTGGAATACAACGGGGCGGCGGAAAGATGATT
ATTGCGAGGCAGGCACCAAGAAGGACAACCTCCATCCTGGAGATGACAGAAACCAGTTTTTCAGATCGTCTCCTTAA
ATAACGATCAACTCCTTAAAGGAGATTTAGACTGCAGCCATTTACACCCCAAATGGGGGCATTAATTACACAG
ACTGCCATATCCCCAACAACATGCGATACTGCAACAGCAGCGTGCCAGACCTGGAGCACTGCCATACGTGACAGC
CAGAGGCCAGCGTTATCAAGGCGGACAATTAGACTCTTGAGAACACACTCGTGTGTGCACATAAAGACACGCAG
ATTACATTTGATAAATGTTACACAGATGCATTTGTGCATTTGAATACTCTGTAATTTATACGGTGTACTATATAA
TGGGATTTAAAAAAAGTGCTATCTTTCTATTTCAAGTTAATTACAAACAGTTTTGTAACTCTTTGCTTTTTAA
TCTT

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FIGURE 350

MGLQTTKWPSHGAFFLKSWLIISLGLYSQVSKLLACPSVCRCDRNFVYCNEERSLTSVPLGIPE
GVTVLYLHNNQINNAGFPAELHNVQSVHTVYLYGNQLDEFFMNLPKNVRVLHLQENNIQTISR
AALAQLLKLEELHLDNSISTVGVEDGAFREAI SLKLLFLSKNHLSSVPVGLPVDLQELRVDE
NRIAVISDMAFQNLTSLERLIVDGNLLTNKGIAEGTFSHLTKLKEFSIVRNSLSHPPDLPGT
HLIRLYLQDNQINHIPLTAFSNLRKLERLDISNNQLRMLTQGVFDNLSNLKQLTARNNPWFCD
CSIKWVTEWLKYIPSSLNVRGFMCGPEQVRGMAVRELMNLLSCPTTTPGLPLFTPAPSTAS
PTTQPPTLSIPNPSRSYTPPTPTTSKLPTIPDWDGRERVTPPISEIRIQLSIHFVNDTSIQVSW
LSLFTVMAYKLTWVKMGHSLVGGIVQERIVSGEKQHLSLVNLEPRSTYRICLVPLDAFNRYRAV
EDTICSEATTHASYLNNGSNTASSHEQTTSHSMGSPFLLAGLIGGAVIFVLVLLSVFCWHMH
KKGRTYSQKWYNRGRRKDDYCEAGTKKDNSILEMTETSFQIVSLNNDQLLKGD FRLQPIYTP
NGGINYTDCHIPNNMRYCNSSVPDLEHCHT

Important features:**Signal peptide:**

amino acids 1-42

Transmembrane domain:

amino acids 542-561

N-glycosylation site.

amino acids 202-206, 298-302, 433-437, 521-525, 635-639, 649-653

Casein kinase II phosphorylation site.

amino acids 204-208, 407-411, 527-531, 593-597, 598-602, 651-655

Tyrosine kinase phosphorylation site.

amino acids 319-328

N-myristoylation site.amino acids 2-8, 60-66, 149-155, 213-219, 220-226, 294-300,
522-528, 545-551, 633-639**Amidation site.**

amino acids 581-585

Leucine zipper pattern.

amino acids 164-186

Phospholipase A2 aspartic acid active site.

amino acids 39-50

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FIGURE 351

AGCCGACGCTGCTCAAGCTGCAACTCTGTTGCAGTTGGCAGTTCCTTTTCGGTTTCCCTCCTGCTGTTTGGGGGCA
TGAAAGGGCTTCGCCGCCGGGAGTAAAGAAGGAATTGACCGGGCAGCGCGAGGGAGGAGCGCGCACGCGACCGC
GAGGGCGGGCGTGACCCCTCGGCTGGAAGTTTGTGCCGGGCCCCGAGCGCGCGCCGGCTGGGAGCTTCGGGTAGA
GACCTAGGCCGCTGGACCGCG**ATG**AGCGCGCCGAGCCTCCGTGCGCGCGCCGCGGGGTTGGGGCTGCTGCTGTGC
GCGGTGCTGGGGCGCGCTGGCCGGTCCGACAGCGCGGTGCGGGGGAACTCGGGCAGCCCTCTGGGGTAGCCGCC
GAGCGCCCATGCCCACTACCTGCCGCTGCCTCGGGGACCTGCTGGACTGCAGTCGTAAGCGGCTAGCGCGTCTT
CCCCAGCCACTCCCGTCCCTGGGTCGCTCGGCTGGACTTAAGTCACAACAGATTATCTTTTCATCAAGGCAAGTTCC
ATGAGCCACCTTCAAAGCCTTCGAGAAGTGAAACTGAACAACAATGAATTGGAGACCATTCCAAATCTGGGACCA
GTCTCGGCAAATATTACACTTCTCTCCTTGGCTGGAAACAGGATTGTTGAAATACTCCCTGAACATCTGAAAGAG
TTTCAGTCCCTTGAAACTTTGGACCTTAGCAGCAACAATATTTTCAGAGCTCCAACTGCATTTCCAGCCCTACAG
CTCAAATATCTGTATCTCAACAGCAACCGAGTCACATCAATGGAACCTGGGTATTTTGACAATTTGGCCAACACA
CTCCTTGTGTTAAAGCTGAACAGGAACCGAATCTCAGCTATCCCACCCAAGATGTTTAAACTGCCCCAACTGCAA
CATCTCGAATTGAACCGAAACAAGATTAAAAATGTAGATGGAGTGACATTCCAAGGCCTTGGTGCTCTGAAGTCT
CTGAAAATGCAAAATAATGGAGTAACGAACTTATGGATGGAGCTTTTGGGGGCTGAGCAACATGGAAATTTTG
CAGCTGGACCATAAACCTAACAGAGATTACCAAGGCTGGCTTTACGGCTTGCTGATGCTGCAGGAACTTCAT
CTCAGCCAAAATGCCATCAACAGGATCAGCCCTGATGCCTGGGAGTTCTGCCAGAAGCTCAGTGAGCTGGACCTA
ACTTTCAATCACTTATCAAGGTTAGATGATTCAAGCTTCCTTGGCCTAAGCTTACTAAATACACTGCACATTGGG
AACAACAGAGTCAGCTACATTGCTGATTGTGCCTTCCGGGGGCTTCCAGTTTAAAGACTTTGGATCTGAAGAAC
AATGAAATTTCTGGACTATTGAAGACATGAATGGTGCTTTCTCTGGGCTTGACAACTGAGGCGACTGATACTC
CAAGGAAATCGGATCCGTTCTATTACTAAAAAAGCCTTCACTGGTTTGGATGCATTGGAGCATCTAGACCTGAGT
GACAACGCAATCATGTCTTTACAAGGCAATGCATTTTCACAAATGAAGAACTGCAACAATTGCATTTAAATACA
TCAAGCCTTTTGTGCGATTGCCAGCTAAAATGGCTCCACAGTGGGTGGCGGAAAACAACCTTTCAGAGCTTTGTA
AATGCCAGTTGTGCCATCCTCAGCTGCTAAAAGGAAGAAGCATTTTTGCTGTTAGCCAGATGGCTTTGTGTGT
GATGATTTTCCCAAACCCAGATCACGGTTCAGCCAGAAACACAGTCGGCAATAAAAGGTTCCAATTTGAGTTTC
ATCTGCTCAGCTGCCAGCAGCAGTGATTCCCCAATGACTTTTGCTTGGAAAAAGACAATGACTACTGCATGAT
GCTGAAATGGAAAATTATGCACACCTCCGGGCCCAAGGTGGCGAGGTGATGGAGTATACCACCATCCTTCGGCTG
CGCGAGGTGGAATTTGCCAGTGAGGGGAAATATCAGTGTGTATCTCCAATCACTTTGGTTCATCCTACTCTGTC
AAAGCCAAGCTTACAGTAAATATGCTTCCCTCATTACCAAGACCCCATGGATCTCACCATCCGAGCTGGGGCC
ATGGCAGCCTTGGAGTGTGCTGCTGTGGGGCACCCAGCCCCCAGATAGCCTGGCAGAAGGATGGGGGCACAGAC
TTCCCAGCTGCACGGGAGAGACGCATGCATGTGATGCCCAGGATGACGTGTTCTTTATCGTGGATGTGAAGATA
GAGGACATTGGGGTATACAGCTGCACAGCTCAGAACAGTGCGAGGAAGTATTTTCAGCAAATGCAACTCTGACTGTC
CTAGAAAACACCATCATTTTTCGGGCCACTGTTGGACCGAACTGTAACCAAGGGAGAAACAGCCGTCCTACAGTGC
ATTGCTGGAGGAAGCCCTCCCCCTAACTGAACTGGACCAAGATGATAGCCCATTTGGTGGTAACCGAGAGGCAC
TTTTTTGCAGCAGGCAATCAGCTTCTGATTATTGTGGACTCAGATGTCAGTGATGCTGGGAAATACACATGTGAG
ATGTCTAACACCCCTTGGCACTGAGAGAGGAAACGTGCGCCTCAGTGTGATCCCCACTCCAACCTGCGACTCCCT
CAGATGACAGCCCCATCGTTAGACGATGACGGATGGGCCACTGTGGGTGTCGTGATCATAGCCGTGGTTTGCTGT
GTGGTGGGCACGTCACTCGTGTGGTGGTTCATCATATACCACACAAGGCGGAGGAATGAAGATTGCAGCATTACC
AACACAGATGAGACCAACTTGCCAGCAGATATTCCTAGTTATTTGTCATCTCAGGGAACGTTAGCTGACAGGCAG
GATGGGTACGTGTCTTCAGAAAGTGGAAGCCACCACAGTTTGTACATCTTCAGGTGCTGGATTTTTCTTACCA
CAACATGACAGTAGTGGGACCTGCCATATTGACAATAGCAGTGAAGCTGATGTGGAAGCTGCCACAGATCTGTTT
CTTTGTCCGTTTTTGGGATCCACAGGCCCTATGTATTTGAAGGGAAATGTGTATGGCTCAGATCCTTTTTGAAACA
TATCATACAGGTTGCAGTCCTGACCAAGAACAGTTTAAATGGACCACTATGAGCCCAGTTACATAAAGAAAAAG
GAGTGCTACCCATGTTCTCATCCTTCAGAAGAATCCTGCGAACGGAGCTTCAGTAATATATCGTGGCCTTCACAT
GTGAGGAAGCTACTTAAACACTAGTTACTCTCACAATGAAGGACCTGGAATGAAAAATCTGTGTCTAAACAAGTCC
TCTTTAGATTTTGTGCAAATCCAGAGCCAGCGTCGGTTGCCTCGAGTAATTCTTTTCATGGGTACCTTTGGAAAA
GCTCTCAGGAGACCTCACCTAGATGCCTATTCAAGCTTTGGACAGCCATCAGATTGTGAGCCAAGAGCCTTTTAT
TTGAAAGCTCATTCTTCCCAGACTTGGACTCTGGGTGAGAGGAAGATGGGAAAGAAAGGACAGATTTTTCAGGAA
GAAATCACATTTGTACCTTTAAACAGACTTTAGAAAATACAGGACTCCAAATTTTCAGTCTTATGACTTGGAC
ACAT**TAG**ACTGAATGAGACCAAGGAAAAGCTTAACTACTACCTCAAGTGAACCTTTATTTAAAGAGAGAGAAT
CTTATGTTTTTTTAAATGGAGTTATGAATTTTAAAGGATAAAAATGCTTTATTTATACAGATGAACCAAAATAC
AAAAAGTTATGAAAATTTTTTATACTGGGAATGATGCTCATATAAGAATACCTTTTTTAACTATTTTTTAACTTTG
TTTTATGCAAAAAGTATCTTACGTAAATTAATGATATAAATCATGATTATTTTATGATTTTTTATAATGCCAGA
TTTCTTTTTTATGGAATAAGTACTAAAGCATTTTTAAATAATACCTGCCTGTACCATTTTTTAAATAGAAGTT
ACTTCATTATATTTTGCACATTATATTTAATAAAATGTGTCAATTTGAAAAAAAAAAAAAAAAAAAAAAAAAAAA

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FIGURE 352

MSAPSLRARAAGLGLLLCAVLGRAGRSDSGGRGELGQPSGVAAERPCPTTCRCLGDLDDCSRKRLARLPEPLPSW
VARLDLSHNRLSFIKASSMSHLQSLREVKLNNNELETIPNLGPVSPANITLLSLAGNRIVEILPEHLKEFQSLETL
DLSSNNISELQTAFFPALQLKYLYLNSNRVTSMEPGYFDNLANTLLVLKLNRRNRI SAIPPKMFKL PQQLHLELNRN
KIKNVDGLTFQGLGALKSLKMQRNGVTKLMDGAFWGLSNMEILQLDHNNLTEITKGWLYGLLMLQELHLSQNAIN
RISPDWEFCQKLSELDLTFNHL SRLDDSSFLGLSLNLT L HIGNNRVSYIADCAFRGLSSLKTLDLKNNEISWTI
EDMNGAFSGLDKLRRLILQGNRIRSITKKAFTGLDALEHLDLSDNAIMSLQGNAFS QMKKLQQLHLNLTSSLLCDC
QLKWLPQWVAENNFQSFVNASCAHPQLLKGRSIFAVSPDGFVCDDFPKPQITVQPETQSAIKGSNLSFICSAASS
SDSPMTFAWKKDNE LLHDAEMENY AHLRAQGGEVMEYTTILRLREVEFASEGKYQCVISNHFGSSYSVKAKLTVN
MLPSFTKTPMDLTIRAGAMARLECAAVGHPAPQIAWQKDG GTDFPAARERRMHVMPEDDVFFIVDVKIEDIGVYS
CTAQNSAGSISANATLTVLETPSFLRPLLDRTVTKGETAVLQCIAGGSPPPKNLWTKDSDPLVVTERHFFAAGNQ
LLIIVDS DVSDAGKYTCEMSNTLGT ERGNVRLSVIPTPTCDSPQMTAPSLDDD GWATVG VV I IAVVCCVVGTSLV
WVVIYHTRRRNEDCSITNTDET NL PADIPS YLSSQGT LADRQDGYVSSESGSHHQFVTSSGAGFFLPQHDSSGT
CHIDNSSEADVEAATDLFLCPFLGSTGPMYLGKNVYGSDPFETYHTGCS PDPRTVLMDHYEPSYIKKKECYPCSH
PSEESCERSFSNISWPSHVRKLLNTSYSHNEGPGMKNLCLNKSSLD F SANPEPASVASSNSFMGTFGKALRRPHL
DAYSSFGQPSDCQPRAFYLKAHSSPDLD SGSEEDGKERTDFQEE NHICTFKQ TLENYRTPNFQSYDLDT

Important features:**Signal sequence:**

amino acids 1-27

Transmembrane domain:

amino acids 808-828

N-glycosylation site.amino acids 122-126, 156-160, 274-278, 442-446, 469-473, 515-519,
688-692, 729-733, 905-909, 987-991, 999-1003, 1016-1020**Glycosaminoglycan attachment site.**

amino acids 886-890

Casein kinase II phosphorylation site.amino acids 99-103, 180-184, 263-267, 314-318, 324-328, 374-378,
383-387, 407-411, 524-528, 608-612, 692-696, 709-713, 731-735,
799-803, 843-847, 863-867, 907-911, 1003-1007, 1018-1022,
1073-1077, 1079-1083, 1081-1085**Tyrosine kinase phosphorylation site.**

amino acids 667-675

N-myristoylation site.amino acids 14-20, 36-42, 239-245, 257-263, 380-386, 427-433,
513-519, 588-594, 672-678, 683-687, 774-780, 933-939**Leucine zipper pattern.**

amino acids 58-80, 65-87

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FIGURE 353

GGGGGTTAGGGAGGAAGGAATCCACCCCCACCCCCCAAACCTTTTCTTCTCCTTTCTGGCTTCGGACATTGG
AGCACTAAATGAACTTGAATTGTGTCTGTGGCGAGCAGGATGGTCGCTGTTACTTTGTGATGAGATCGGGGATGA
ATTGCTCGCTTTAAAAATGCTGCTTTGGATTCTGTTGCTGGAGACGTCTCTTTGTTTTGCCGCTGGAAACGTTAC
AGGGGACGTTTGC AAAGAGAAGATCTGTTCTGCAATGAGATAGAAGGGGACCTACACGTAGACTGTGAAAAAA
GGGCTTCACAAGTCTGCAGCGTTTCACTGCCCCGACTTCCAGTTTACCATTTATTTCTGCATGGCAATTCCCT
CACTCGACTTTTCCCTAATGAGTTCGCTAACTTTTATAATGCGGTTAGTTTGCACATGGAAAACAATGGCTTGCA
TGAAATCGTTCCGGGGGCTTTTCTGGGGCTGCAGCTGGTGAAAAGGCTGCACATCAACAACAACAAGATCAAGTC
TTTTCGAAAGCAGACTTTTCTGGGGCTGGACGATCTGGAATATCTCCAGGCTGATTTTAATTTATTACGAGATAT
AGACCCGGGGGCTTCCAGGACTTGAACAAGCTGGAGGTGCTCATTTTAAATGACAATCTCATCAGCACCTTACC
TGCCAACGTGTTCCAGTATGTGCCATCACCCACCTCGACCTCCGGGGTAACAGGCTGAAAACGCTGCCCTATGA
GGAGGTCTTGGAGCAAATCCCTGGTATTGCGGAGATCCTGCTAGAGGATAACCTTGGGACTGCACCTGTGATCT
GCTCTCCCTGAAAGAATGGCTGGAAAACATTCCCAAGAATGCCCTGATCGGCCGAGTGGTCTGCGAAGCCCCCAC
CAGACTGCAGGGTAAAGACCTCAATGAAACCACCGAACAGGACTTGTGTCTTTGAAAACCGAGTGGATTCTAG
TCTCCCGCGCCCCCTGCCCAAGAAGAGACCTTTGCTCCTGGACCCCTGCCAATCCTTTCAAGACAAATGGGCA
AGAGGATCATGCCACACCAGGGTCTGCTCCAAACGGAGGTACAAAGATCCCAGGCAACTGGCAGATCAAAATCAG
ACCCACAGCAGCGATAGCGACGGGTAGCTCCAGGAACAAACCTTAGCTAACAGTTTACCCTGCCCTGGGGGCTG
CAGCTGCGACCACATCCCAGGGTCGGGTTTAAAGATGAACTGCAACAACAGGAACGTGAGCAGCTTGGCTGATTT
GAAGCCCAAGCTCTCTAACGTGCAGGAGCTTTTCTACGAGATAACAAGATCCACAGCATCCGAAAATCGCACTT
TGTGGATTACAAGAACCTCATTTCTGTTGGATCTGGGCAACAATAACATCGCTACTGTAGAGAACAACACTTTCAA
GAACCTTTTGGACCTCAGGTGGCTATACATGGATAGCAATTACCTGGACACGCTGTCCCGGGAGAAATTCGCGGG
GCTGCAAAACCTAGAGTACCTGAACGTGGAGTACAACGCTATCCAGCTCATCTCCCGGGCACTTTCAATGCCAT
GCCCAAACCTGAGGATCCTCATTTCTCAACAACAACCTGCTGAGGTCCCTGCCTGTGGACGTGTTGCTGGGGTCTC
GCTCTCTAAACTCAGCCTGCACAACAATTACTTCATGTACCTCCCGGTGGCAGGGGTGCTGGACCAGTTAACCTC
CATCATCCAGATAGACCTCCACGGAAACCCCTGGGAGTGCTCCTGCACAATTGTGCCTTTCAAGCAGTGGGCAGA
ACGCTTGGGTTCCGAAGTGCTGATGAGCGACCTCAAGTGTGAGACGCCGGTGAACCTCTTTAGAAAGGATTTTCAT
GCTCCTCTCCAATGACGAGATCTGCCCTCAGCTGTACGCTAGGATCTCGCCACGTTAACCTTCGCACAGTAAAAA
CAGCACTGGGTTGGCGGAGACCGGGACGCACTCCAATCCTACCTAGACACCAGCAGGGTGTCCATCTCGGTGTT
GGTCCCGGGACTGCTGCTGGTGTGTTGTACCTCCGCCTTACCGTGGTGGGCATGCTCGTGTGTTATCCTGAGGAA
CCGAAAGCGGTCCAAGAGACGAGATGCCAATCCTCCGCGTCCGAGATTAATTCCTACAGACAGTCTGTGACTC
TTCCTACTGGCACAATGGGCCTTACAACGCAGATGGGGCCACAGAGTGTATGACTGTGGCTCTCACTCGCTCTC
AGACTAAGACCCCCAACCCCAATAGGGGAGGGCAGAGGGAAGGCGATACATCCTTCCCCACCGCAGGCACCCCGG
GGCTGGAGGGGCGTGTAACCAATCCCGCGCCATCAGCCTGGATGGGCATAAGTAGATAAATAACTGTGAGCTC
GCACAACCGAAAGGGCCTGACCCCTTACTTAGCTCCCTCCTTGAAACAAAGAGCAGACTGTGGAGAGCTGGGAGA
GCGCAGCCAGCTCGCTCTTTGCTGAGAGCCCTTTTGACAGAAAAGCCAGCACGACCCTGCTGGAAGAAGTACA
GTGCCCTCGCCCTCGGCCCGGGCCTGTGGGGTTGGATGCCGCGTTCTATACATATATACATATATCCACATC
TATATAGAGAGATAGATATCTATTTTCCCCTGTGGATTAGCCCCGTGATGGCTCCCTGTTGGCTACGCAGGGAT
GGGCAGTTGCACGAAGGCATGAATGTATTGTAAATAAGTAACTTTGACTTCTGAC

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FIGURE 354

MLLWILLLETSLCFAAGNVTGDVCKEKICSCNEIEGDLHVDCEKKGFTSLQRFTAPTSQFYHL
FLHGNSLTRLPNEFANFYNAVSLHMENNGLHEIVPGAFLGLQLVKRLHINNNKIKSFRKQTF
LGLDDLEYLQADFNLLRDIDPGAQDLNKLVLILNDNLISTLPANVFQYVPITHLDLRGNRL
KTLPEEVLEQIPGIAEILLEDNPWDCTCDLLSLKEWLENIPKNALIGRVVCEAPTRLQGKDL
NETTEQDLCPLKNRVDSSLPAPPAQEETFAPGPLPTPFKTNGQEDHATPGSAPNGGTKIPGNW
QIKIRPTAAIATGSSRNKPLANSRPCPGGCSCDHIPGSGLKMNCCNNRVSSLADLKPKLSNVQ
ELFLRDNKIHSIRKSHFVDYKNLILLDLGNNNIATVENNTFKNLLDLRWLYMDSNYLDTLSRE
KFAGLQNLLEYLNVEYNAIQILILPGTFNAMPKLRILILNNNLLRSLPVDVFAGVSLSKLSLHNN
YFMYLPVAGVLDQLTSIIQIDLHGPNWECSTIVPFKQWAERLGSEVLMSDLKCETPVNFFRK
DFMLLSNDEICPQLYARISPTLTSHSKNSTGLAETGTHSNSYLDTSRVSISVLVPGLLLVFVT
SAFTVVGMLVFILNRNRKRSKRDRANDSSASEINSLQTVCDSSYWHNGPYNADGAHRVYDCGSHS
LSD

Important features:**Signal sequence:**

amino acids 1-15

Transmembrane domain:

amino acids 618-638

N-glycosylation site.

amino acids 18-22, 253-257, 363-367, 416-420, 595-599, 655-659

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 122-126, 646-650

Casein kinase II phosphorylation site.amino acids 30-34, 180-184, 222-226, 256-260, 366-370, 573-577,
608-612, 657-661, 666-670, 693-697**N-myristoylation site.**amino acids 17-23, 67-73, 100-106, 302-308, 328-334, 343-349,
354-360, 465-471, 493-499, 598-604, 603-609**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 337-348

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FIGURE 355

AGTCGACTGCGTCCCCTGTACCCGGCGCCAGCTGTGTTCTGACCCCAGAATAACTCAGGGCTGCACCGGGCCTG
GCAGCGCTCCGCACACATTTCTGTGCGGGCCTAAGGGAAACTGTTGGCCGCTGGGCCCCGGGGGGATTCTTGG
CAGTTGGGGGGTCCGTGCGGAGCGAGGGCGGAGGGGAAGGGAGGGGAACCGGGTTGGGGAAGCCAGCTGTAGAG
GGCGGTGACCGCGCTCCAGACACAGCTCTGCGTCCTCGAGCGGGACAGATCCAAGTTGGGAGCAGCTCTGCGTGC
GGGGCCTCAGAGA**ATG**AGGCCGGCGTTGCGCCTGTGCCTCCTCTGGCAGGCGCTCTGGCCCCGGGCCGGCGGCGG
CGAACACCCCACTGCCGACCGTGCTGGCTGCTCGGCCTCGGGGGCCTGCTACAGCCTGCACCACGCTACCATGAA
GCGGCAGGCGGCCGAGGAGGCCTGCATCCTGCGAGGTGGGGCGCTCAGCACCGTGCGTGCGGGCGCCGAGCTGCG
CGCTGTGCTCGCGCTCCTGCGGGCAGGCCCAGGGCCCCGAGGGGGGCTCCAAAGACCTGCTGTTCTGGGTGCGACT
GGAGCGCAGGCGTTCCCACTGCACCCTGGAGAACGAGCCTTTGCGGGGTTTCTCCTGGCTGTCTCCGACCCCGG
CGGTCTCGAAAGCGACACGCTGCAGTGGGTGGAGGAGCCCCAACGCTCCTGCACCGCGCGGAGATGCGCGGTACT
CCAGGCCACCGGTGGGGTCGAGCCCGCAGGCTGGAAGGAGATGCGATGCCACCTGCGCGCCAACGGCTACCTGTG
CAAGTACCAGTTTGAGGTCTTGTGTCCTGCGCCGCGCCCCGGGGCCGCTCTAACTTGAGCTATCGCGCGCCCTT
CCAGCTGCACAGCGCCGCTCTGGACTTCAGTCCACCTGGGACCGAGGTGAGTGCCTCTGCCGGGACAGCTCCC
GATCTCAGTTACTTGATCGCGGACGAAATCGGCGCTCGCTGGGACAACTCTCGGGCGATGTGTTGTGTCCTG
CCCCGGGAGGTACCTCCGTGCTGGCAAATGCGCAGAGCTCCCTAACTGCCTAGACGACTTGGGAGGCTTTGCCTG
CGAATGTGCTACGGGCTTCGAGCTGGGGAAGGACGGCCGCTCTTGTGTGACCAGTGGGGAAGGACAGCCGACCCT
TGGGGGGACCGGGGTGCCACCAGGCGCCCGCCGGCCACTGCAACCAGCCCCGTGCCGCAGAGAACATGGCCAAT
CAGGGTGCAGGAGAAGCTGGGAGAGACACCACTTGTCCCTGAACAAGACAATTACAGTAACATCTATTCTGAGAT
TCCTCGATGGGGATCACAGAGCACGATGTCTACCCTTCAAATGTCCCTTCAAGCCGAGTCAAAGGCCACTATCAC
CCCATCAGGGAGCGTGATTTCCAAGTTTAATTCTACGACTTCCTCTGCCACTCCTCAGGCTTTGACTCCTCCTC
TGCCGTGGTCTTCATATTTGTGAGCACAGCAGTAGTAGTGTGGTGATCTTGACCATGACAGTACTGGGGCTTGT
CAAGCTCTGCTTTCACGAAAGCCCCCTCTTCCCAGCCAAGGAAGGAGTCTATGGGCCCCGGGGCCTGGAGAGTGA
TCCTGAGCCCGCTGCTTTGGGCTCCAGTTCTGCACATTGCACAAACAATGGGGTGAAAGTCGGGGACTGTGATCT
GCGGGACAGAGCAGAGGGTGCTTGCTGGCGGAGTCCCCTCTTGGCTCTAGTGATGCAT**AG**GGGAAACAGGGGACA
TGGGCACTCCTGTGAACAGTTTTTCACTTTTGATGAAACGGGGGAACCAAGAGGAACCTTACTTGTGTAACCTGACAA
TTTCTGCAGAAATCCCCCTTCTCTAAATTCCTTTACTCCACTGAGGAGCTAAATCAGAACTGCACACTCCTTC
CCTGATGATAGAGGAAGTGGAAGTGCCTTTAGGATGGTGATACTGGGGGACCGGGTAGTGCTGGGGAGAGATATT
TTCTTATGTTTATTTCGGAGAATTTGGAGAAGTGATTGAACTTTTCAAGACATTGGAAACAAATAGAACACAATAT
AATTTACATTAAAAAATAATTTCTACCAAATGGAAAGGAAATGTTCTATGTTGTTTCAAGGCTAGGAGTATATTGG
TTCGAAATCCCAGGGAAAAAATAAAAAATAAAAAATTAAAGGATTGTTGAT

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FIGURE 356

MRPAFALCLLWQALWPGPGGGEHPTADRAGCSASGACYSLHHATMKRQAAEEACILRGGALST
VRAGAE LRAVLALLRAGPGPGGGSKDLLFWVALERRRSHCTLENEPLRGFSWLSSDPGGLESD
TLQWVEEPQRSCTARRCAVLQATGGVEPAGWKEMRCHLRANGYLCKYQFEVLC PAPRPGAASN
LSYRAPFQLHSAALDFSPPGTEVSALCRGQLPISVTCIADEIGARWDKLSGDVLCPCPGRYLR
AGKCAELPNCLDDLGGFACECATGFELGKDGRSCVTSGEGQPTLGGTGVPTRRPPATATSPVP
QRTWPIRVDEKLGETPLVPEQDNSVTSIPEIPRWGSQSTMSTLQMSLQAESKATITPSGSVIS
KFNSTTSSATPQAFDSSSAVVFI FVSTAVVVLVILTM TVLGLVKLCFHESPSSQPRKESMGPP
GLESDPEPAALGSSSAHCTNNGVKVGDCDLRDRAEGALLAESPLGSSDA

Important features:**Signal sequence:**

amino acids 1-16.

Transmembrane domain:

amino acids 399-418

N-glycosylation site.

amino acids 189-193, 381-385

Glycosaminoglycan attachment site.

amino acids 289-293

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 98-102, 434-438

Casein kinase II phosphorylation site.

amino acids 275-279, 288-292, 342-346, 445-449

N-myristoylation site.amino acids 30-36, 35-41, 58-64, 59-65, 121-127, 151-157,
185-191, 209-215, 267-273, 350-356, 374-380, 453-459, 463-469,
477-483**Aspartic acid and asparagine hydroxylation site.**

amino acids 262-274

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FIGURE 357

CCCATCTCAAGCTGATCTTGGCACCTCTCATGCTCTGCTCTCTTCAACCAGACCTCTACATTCCATTTTGAAGA
AGACTAAAAATGGTGTTCCTAATGTGGACACTGAAGAGACAAATCTTATCCTTTTTTAACATAATCCTAATTTCC
AAACTCCTTGGGGCTAGATGGTTTCCTAAAACCTCTGCCCTGTGATGTCACCTCTGGATGTTCCAAAGAACCATGTG
ATCGTGGACTGCACAGACAAGCATTGACAGAAATTCCTGGAGGTATTCACGACACACCACGAACCTCACCCCTC
ACCATTAACCACATACCAGACATCTCCCCAGCGTCCTTTCACAGACTGGACCATCTGGTAGAGATCGATTTTCAGA
TGCAACTGTGTACCTATTCACCTGGGGTCAAAAAACAACATGTGCATCAAGAGGCTGCAGATTAAACCCAGAAAGC
TTTAGTGGACTCACTTATTTAAAATCCCTTTACCTGGATGGAAACCAGCTACTAGAGATACCGCAGGGCCTCCCG
CCTAGCTTACAGCTTCTCAGCCTTGAGGCCAACACATCTTTTCCATCAGAAAAGAGAATCTAACAGAACTGGCC
AACATAGAAATACTCTACCTGGGCCAAAACCTGTTATTATCGAAATCCTTGTTATGTTTTCATATTCAATAGAGAAA
GATGCCTTCCTAAACTTGACAAAAGTTAAAAGTGCTCTCCCTGAAAGATAACAATGTCACAGCCGTCCCTACTGTT
TTGCCATCTACTTTAACAGAACTATATCTCTACAACAACATGATTGCAAAAATCCAAGAAGATGATTTTAATAAC
CTCAACCAATTACAAATTCTTGACCTAAGTGGAAATTGCCCTCGTTGTTATAATGCCCCATTTCTTTGTGCGCCG
TGTA AAAATAATTCTCCCTACAGATCCCTGTAATGCTTTTGATGCGCTGACAGAATTAAGTTTACGTCTA
CACAGTAACCTCTCTCAGCATGTGCCCCAAGATGGTTTAAAGAACATCAACAAACTCCAGGAACCTGGATCTGTCC
CAAACTTCTTGGCCAAAAGAAATTGGGGATGCTAAATTTCTGCATTTTCTCCCGAGCCTCATCCAATTGGATCTG
TCTTTCAATTTTGAACCTCAGGTCTATCGTGCATCTATGAATCTATCACAAGCATTTTCTTCACTGAAAAGCCTG
AAAATTCTGCGGATCAGAGGATATGTCTTTAAAGAGTTGAAAAGCTTTAACCTCTCGCCATTACATAATCTTCAA
AATCTTGAAGTTCTTGATCTTGGCACTAATTTATAAAAATTGCTAACCTCAGCATGTTTAAACAATTTAAAAGA
CTGAAAGTCATAGATCTTTCAGTGAATAAAATATCACCTTCAGGAGATTCAAGTGAAGTTGGCTTCTGCTCAAAT
GCCAGAACTTCTGTAGAAAGTTATGAACCCAGGTCTTGAACAATTACATTATTTTCAGATATGATAAGTATGCA
AGGAGTTGCAGATTCAAAAACAAAGAGGCTTCTTTCATGTCTGTTAATGAAAGCTGCTACAAGTATGGGCAGACC
TTGGATCTAAGTAAAAATAGTATATTTTTTGTCAAGTCTCTGATTTTCAGCATCTTTCTTTCTCAAATGCCTG
AATCTGTGAGGAAATCTCATTAGCCAACTCTTAATGGCAGTGAATTTCAACCTTTAGCAGAGCTGAGATATTTG
GACTTCTCCAACAACCGGCTTGATTTACTCCATTCAACAGCATTTGAAGAGCTTCACAACTGGAAGTTCTGGAT
ATAAGCAGTAATAGCCATTATTTCAATCAGAAGGAATTACTCATATGCTAACTTTACCAAGAACCTAAAGGTT
CTGCAGAAACTGATGATGAACGACAATGACATCTCTTCTCCACCAGCAGGACCATGGAGAGTGAGTCTCTTAGA
ACTCTGGAATTGAGAGGAAATCACTTAGATGTTTTATGGAGAGAAGGTGATAACAGATACTTACAATTATTCAAG
AATCTGCTAAAATTAGAGGAATTAGACATCTCTAAAAATTCCTAAGTTTCTTGCCTTCTGGAGTTTTTGTGGT
ATGCCTCAAATCTAAAGAATCTCTCTTTGGCCAAAATGGGCTCAAATCTTTCAGTTGGAAGAACTCCAGTGT
CTAAAGAACCTGGAACCTTTGGACCTCAGCCACAACCAACTGACCACTGTCCCTGAGAGATTATCCAACCTGTTCC
AGAAGCCTCAAGAATCTGATCTTAAAGAATAATCAAATCAGGAGTCTGACGAAGTATTTTCTACAAGATGCCTTC
CAGTTGCGATATCTGGATCTCAGCTCAAATAAAATCCAGATGATCCAAAAGACCAGCTTCCAGAAAATGTCTTC
AACAATCTGAAGATGTTGCTTTTGCATCATAATCGGTTTCTGTGCACCTGTGATGCTGTGTGGTTTGTCTGGTGG
GTTAACCATACGGAGGTGACTATTCCTTACCTGGCCACAGATGTGACTTGTGTGGGGCCAGGAGCACACAAGGGC
CAAAGTGTGATCTCCCTGGATCTGTACACCTGTGAGTTAGATCTGACTAACCTGATTCTGTTCTCACTTTCCATA
TCTGTATCTCTCTTTCTCATGGTGATGATGACAGCAAGTCACCTCTATTTCTGGGATGTGTGGTATATTTACCAT
TTCTGTAAGGCCAAGATAAAGGGGTATCAGCGTCTAATATCACCAGACTGTTGCTATGATGCTTTTATTGTGTAT
GACACTAAAGACCCAGCTGTGACCGAGTGGGTTTTGGCTGAGCTGGTGGCCAACTGGAAGACCCAAGAGAGAAA
CATTTTAATTTATGTCTCGAGGAAAAGGACTGGTTACCAGGGCAGCCAGTTCTGGAAAACCTTTCCAGAGCATA
CAGCTTAGCAAAAAGACAGTGTGTGTGATGACAGACAAGTATGCAAAGACTGAAAATTTTAAGATAGCATTTTAC
TTGTCCCATCAGAGGCTCATGGATGAAAAAGTTGATGTGATTATCTTGATATTTCTTGAGAAGCCCTTTTCAGAAG
TCCAAGTTCTCCAGCTCCGGAAGGCTCTGTGGGAGTTCTGTCTTGTGAGTGGCCAAACAAACCCGCAAGCTCAC
CCATACTTCTGGCAGTGTCTAAAGAACGCCCTGGCCACAGACAATCATGTGGCCTATAGTCAGGTGTTCAAGGAA
ACGGTCTAGCCCTTCTTTGCAAAACACAACCTGCCTAGTTTACCAAGGAGAGGCTGGC

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FIGURE 358

MVFPMWTLKRQILILFNIIILISKLLGARWFPKTLPCDVTLDVPKNHVIVDCTDKHLTEIPGGI
PTNTTNLTLTINHIPDISPASFHRLDHLVEIDFRNCNCPVPIPLGSKNNMCIKRLQIKPRSFSGL
TYLKSLYLDGNQLLEIPQGLPPSLQLLSLEANNIFSIRKENLTELANIEIILYLGQNCYYRNP
YVSYSEKDAFLNLTKLKVLSLKDNNVTAVPTVLPSTLTELYLYNNMIAKIQEDDFNNLNQLQ
ILDLSGNCPRCYNAPFPCAPCKNNSPLQIPVNAFDALTELKVLRLHSNSLQHVPFRWFKNINK
LQELDLSQNFLAKEIGDAKFLHFLPSLIQLDLSFNFELOVYRASMNLSQAFSSLKSLKILRIR
GYVFKELKSFNLSPLHNLQNLEVLDTGNTFIKIANLSMFKQFKRLKVIDLSVNKISPSGDSSE
VGFCSNARTSVESYEPQVLEQLHYFRYDKYARSCRFKNKEASFMSVNESCYKYGQTLDSLKNS
IFFVKSSDFQHLSFLKCLNLSGNLISQTLNGSEFQPLAELRYLDFSNRDLHSTAFEELHK
LEVLDISSNSHYFQSEGITHMLNFTKNLKVLOKLMMNDNDISSSTSRTESESLRTLEFRGNH
LDVLWREGDNRYLQLFKNLLKLEELDISKNLSLFLPSGVFDGMPPNLKNLSLAKNGLKSFSWK
KLQCLKNLETLDLSHNQLTTVPERLSNCSRSLKNLILKNNQIRSLTKYFLQDAFQLRYLDLSS
NKIQMIQKTSFPENVLNNLKMLLLHHNRFLCTCDVWFVWVWNHTEVTIPYLATDVTCVGP
HKGQSVISLDLYTCELDLTNLILFSLSISVSLFLMVMMTASHLYFWDVWYIYHFCKAKIKGYQ
RLISPDCCYDAFIVYDTKDPVTEWVLAELVAKLEDPREKHFNLCLEERDWLPGQPVLENLSQ
SIQLSKKTVFVMTDKYAKTENFKIAFYLSHQRLMDEKVDVILIFLEKPFQKSKFLQLRKRLC
GSSVLEWPTNPQAHFYFWQCLKNALATDNHVAYSQVFKETV

Important features:**Signal sequence:**

amino acids 1-26

Transmembrane domain:

amino acids 840-860

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FIGURE 359

GACGGCTGGCCACCATGCACGGCTCCTGCAGTTTCCTGATGCTTCTGCTGCCGCTACTGCTAC
TGCTGGTGGCCACCACAGGCCCCGTTGGAGCCCTCACAGATGAGGAGAAACGTTTGATGGTGG
AGCTGCACAACCTCTACCGGGCCCAGGTATCCCCGACGGCCTCAGACATGCTGCACATGAGAT
GGGACGAGGAGCTGGCCGCCTTCGCCAAGGCCTACGCACGGCAGTGCGTGTGGGGCCACAACA
AGGAGCGCGGGCGCCGCGGCGAGAATCTGTTTCGCCATCACAGACGAGGGCATGGACGTGCCGC
TGGCCATGGAGGAGTGGCACCACGAGCGTGAGCACTACAACCTCAGCGCCGCCACCTGCAGCC
CAGGCCAGATGTGCGGCCACTACACGCAGGTGGTATGGGCCAAGACAGAGAGGATCGGCTGTG
GTTCCCACCTTCTGTGAGAAGCTCCAGGGTGTGAGGAGACCAACATCGAATTACTGGTGTGCA
ACTATGAGCCTCCGGGGAACGTGAAGGGGAAACGGCCCTACCAGGAGGGGACTCCGTGCTCCC
AATGTCCCTCTGGCTACCACTGCAAGAACTCCCTCTGTGAACCCATCGGAAGCCCGGAAGATG
CTCAGGATTTGCCTTACCTGGTAACTGAGGCCCATCCTTCCGGGCGACTGAAGCATCAGACT
CTAGGAAAATGGGTACTCCTTCTTCCCTAGCAACGGGGATTCCGGCTTTCTTGGTAACAGAGG
TCTCAGGCTCCCTGGCAACCAAGGCTCTGCCTGCTGTGGAAACCCAGGCCCCAACTTCCTTAG
CAACGAAAGACCCGCCCTCCATGGCAACAGAGGCTCCACCTTGCGTAACAACCTGAGGTCCCTT
CCATTTTGGCAGCTCACAGCCTGCCCTCCTTGGATGAGGAGCCAGTTACCTTCCCCAAATCGA
CCCATGTTCCCTATCCCCAAAATCAGCAGACAAAGTGACAGACAAAACAAAAGTGCCCTCTAGGA
GCCCAGAGAACTCTCTGGACCCCAAGATGTCCCTGACAGGGGCAAGGGAACTCCTACCCCATG
CCCAGGAGGAGGCTGAGGCTGAGGCTGAGTTGCCTCCTTCCAGTGAGGTCTTGGCCTCAGTTT
TTCCAGCCCAGGACAAGCCAGGTGAGCTGCAGGCCACACTGGACCACACGGGGCACACCTCCT
CCAAGTCCCTGCCCAATTTCCCCAATACCTCTGCCACCGCTAATGCCACGGGTGGGCGTGCCC
TGGCTCTGCAGTCGTCCTTGCCAGGTGCAGAGGGCCCTGACAAGCCTAGCGTTGTGTCAGGGC
TGAATCGGGCCCTGGTCATGTGTGGGGCCCTCTCCTGGGACTACTGCTCCTGCCTCCTCTGG
TGTTGGCTGGAATCTTCTTGAATGGGATACCACTCAAAGGGTGAAGAGGTCAGCTGTCCTCCTG
TCATCTTCCCCACCCTGTCCCCAGCCCCTAAACAAGATACTTCTTGGTTAAGGCCCTCCGGAA
GGGAAAGGCTACGGGGCATGTGCCTCATCACACCATCCATCCTGGAGGCACAAGGCCTGGCTG
GCTGCGAGCTCAGGAGGCCGCCTGAGGACTGCACACCGGGCCACACCTCTCCTGCCCTCCC
TCCTGAGTCCTGGGGGTGGGAGGATTTGAGGGAGCTCACTGCCTACCTGGCCTGGGGCTGTCT
GCCACACAGCATGTGCGCTCTCCCTGAGTGCCTGTGTAGCTGGGGATGGGGATTCTAGGGG
CAGATGAAGGACAAGCCCCACTGGAGTGGGGTTCTTTGAGTGGGGAGGCAGGGACGAGGGAA
GGAAAGTAACTCCTGACTCTCCAATAAAAACCTGTCCAACCTGTGAAA

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FIGURE 360

MHGSCSFLMLLLPLLLLLLVATTGPVGALTDEEKRLMVELHNLRYAQVSPTASDMLHMRWDEEL
AAFAKAYARQCVWGHNKERGRGENLFAITDEGMDVPLAMEEWHHEREHYNLSAATCSPGQMC
GHYTQVWAKTERIGCGSHFCEKLQGVETNIELLVCNYEPPGNVKGKRPHYQEGTPCSQCPSG
YHCKNSLCEPIGSPEDAQDLPYLVTEAPSFRAATEASDSRKMGTPSSLATGIPAFVLVTEVSGSL
ATKALPAVETQAPTSLATKDPPSMATEAPPCVTTEVP SILAAHSLPSLDEEPVTFPKSTHVPI
PKSADKVTDKTKVPSRSPENSLDPKMSLTGARELLPHAQEEAEAEALPPSSEVLASVFPAQD
KPGELQATLDHTGHTSSKSLPNFPNTSATA¹NATGGRALALQSSLPGAEGPDKPSVVSGLN²SGP
GHVWGPLLGLLLLPPPLVL³AGIF

Important features:**Signal sequence:**

amino acids 1-22

N-glycosylation site.

amino acids 114-118, 403-407, 409-413

Glycosaminoglycan attachment site.

amino acids 439-443

Casein kinase II phosphorylation site.

amino acids 29-33, 50-54, 156-160, 195-199, 202-206, 299-303

N-myristoylation site.

amino acids 123-129, 143-149, 152-158, 169-175, 180-186, 231-237, 250-256

Amidation site.

amino acids 82-86, 172-176

Peroxidases proximal heme-ligand signature.

amino acids 287-298

Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7 signature 1.

amino acids 127-138

Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7 signature 2.

amino acids 160-172

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FIGURE 361

GACTAGTTCTCTTGGAGTCTGGGAGGAGGAAAGCGGAGCCGGCAGGGAGCGAACCAGGACTGG
GGTGACGGCAGGGCAGGGGGCGCCTGGCCGGGGAGAAGCGCGGGGGCTGGAGCACCACCAACT
GGAGGGTCCGGAGTAGCGAGCGCCCCGAAGGAGGCCATCGGGGAGCCGGGAGGGGGGACTGCG
AGAGGACCCCGGCGTCCGGGCTCCCGGTGCCAGCGCT**ATG**AGGCCACTCCTCGTCCTGCTGCT
CCTGGGCCTGGCGGCCGGCTCGCCCCACTGGACGACAACAAGATCCCCAGCCTCTGCCCCGGG
GCACCCCGGCCCTTCCAGGCACGCCGGGCCACCATGGCAGCCAGGGCTTGCCGGGCCGCGATGG
CCGCGACGGCCGCGACGGCGCGCCCGGGGCTCCGGGAGAGAAAGGCGAGGGCGGGAGGCCGGG
ACTGCCGGGACCTCGAGGGGACCCCGGGCCGCGAGGAGAGGCGGGACCCGCGGGGGCCCACCGG
GCCTGCCGGGGAGTGCTCGGTGCCTCCGCGATCCGCCTTCAGCGCCAAGCGCTCCGAGAGCCG
GGTGCTCCGCCGTCTGACGCACCCTTGCCCTTCGACCGCGTGCTGGTGAACGAGCAGGGACA
TTACGACGCCGTCACCGGCAAGTTACCTGCCAGGTGCCTGGGGTCTACTACTTCGCCGTCCA
TGCCACCGTCTACCGGGCCAGCCTGCAGTTTGATCTGGTGAAGAATGGCGAATCCATTGCCTC
TTTCTTCCAGTTTTTTCGGGGGGTGGCCCAAGCCAGCCTCGCTCTCGGGGGGGGCCATGGTGAG
GCTGGAGCCTGAGGACCAAGTGTGGGTGCAGGTGGGTGTGGGTGACTACATTGGCATCTATGC
CAGCATCAAGACAGACAGCACCTTCTCCGATTTCTGGTGTACTCCGACTGGCACAGCTCCCC
AGTCTTTGCT**TAG**TGCCCCACTGCAAAGTGAGCTCATGCTCTCACTCCTAGAAGGAGGGTGTGA
GGCTGACAACAGGTCATCCAGGAGGGCTGGCCCCCTGGAATATTGTGAATGACTAGGGAGG
TGGGGTAGAGCACTCTCCGTCCTGCTGCTGGCAAGGAATGGGAACAGTGGCTGTCTGCGATCA
GGTCTGGCAGCATGGGGCAGTGGCTGGATTTCTGCCCAAGACCAGAGGAGTGTGCTGTGCTGG
CAAGTGTAAGTCCCCCAGTTGCTCTGGTCCAGGAGCCCACGGTGGGGTGCTCTCTTCTGGTC
CTCTGCTTCTCTGGATCCTCCCCACCCCTCCTGCTCCTGGGGCCGGCCCTTTTCTCAGAGAT
CACTCAATAAACCTAAGAACCCTCATAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

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FIGURE 362

MRPLLVLALLGLAAGSPPLDDNKIPSLCPGHPGLPGTPGHHGSQGLPGRDGRDGRDGAPGAPG
EKGEGRPGPLPGPRGDPGPRGEAGPAGPTGPAGECSVPPRSAFSAKRSESRVPPPSDAPLPFD
RVLVNEQGHYDAVTGKFTCQVPGVYYFAVHATVYRASLQFDLVKNGESIÄSFFQFFGGWPKPA
SLSGGAMVRLEPEDQVWVQVGVDYIGIYASIKTDSTFSGFLVYSDWHSSPVFA

Important features:**Signal sequence.**

amino acids 1-15

N-myristoylation sites.

amino acids 11-17, 68-74, 216-222

Cell attachment sequence.

amino acids 77-80

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FIGURE 363

[illegible]

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FIGURE 364

MMWRPSVLLLLLLLLLRHGAQGKPSPDAGPHGQGRVHQAAPLSDAPHDDAHGNFQYDHEAFLGRE
VAKEFDQLTPEESQARLGRIVDRMDRAGDGDGWVSLAELRAWIAHTQQRHIRDSVSAAWDTYD
TDRDGRVGWEELRNATYGHYAPGEEFHDVEDAETYKKMLARDERRFRVADQDGD SMATREELT
AFLHPEEFPHMRDIVIAETLEDLDRNKDGYVQVEEYIADLYSAEPGEEEPAWVQTERQQFRDF
RDLNKDGHLDGSEVGHWVLPPAQDQPLVEANHLLHESD TDKDGRLSKAEILGNWNMFVGSQAT
NYGEDLTRHHDEL

Important features:**Signal sequence:**

amino acids 1-20

N-glycosylation site.

amino acids 140-144

Casein kinase II phosphorylation site.amino acids 72-76, 98-102, 127-131, 184-188, 208-212, 289-293,
291-295, 298-302**N-myristoylation site.**

amino acids 263-269, 311-317

Endoplasmic reticulum targeting sequence.

amino acids 325-330

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FIGURE 365

GTCTGTTCCCAGGAGTCCTTCGGCGGCTGTTGTGTCAGTGGCCTGATCGCG**ATG**GGGACAAAG
GCGCAAGTCGAGAGGAAACTGTTGTGCCTCTTCATATTGGCGATCCTGTTGTGCTCCCTGGCA
TTGGGCAGTGTTACAGTGCACCTCTTCTGAACCTGAAGTCAGAATTCCTGAGAATAATCCTGTG
AAGTTGTCCTGTGCCTACTCGGGCTTTTCTTCTCCCCGTGTGGAGTGGAAGTTTGACCAAGGA
GACACCACCAGACTCGTTTGCTATAATAACAAGATCACAGCTTCCTATGAGGACCGGGTGACC
TTCTTGCCAACTGGTATCACCTTCAAGTCCGTGACACGGGAAGACACTGGGACATACACTTGT
ATGGTCTCTGAGGAAGGCGGCAACAGCTATGGGGAGGTCAAGGTCAAGCTCATCGTGCTTGTG
CCTCCATCCAAGCCTACAGTTAACATCCCCTCCTCTGCCACCATTTGGGAACCGGGCAGTGCTG
ACATGCTCAGAACAAGATGGTTCCCCACCTTCTGAATACACCTGGTTCAAAGATGGGATAGTG
ATGCCTACGAATCCCAAAGCACCCGTGCCTTCAGCAACTCTTCCTATGTCCTGAATCCCACA
ACAGGAGAGCTGGTCTTTGATCCCCTGTCAGCCTCTGATACTGGAGAATACAGCTGTGAGGCA
CGGAATGGGTATGGGACACCCATGACTTCAAATGCTGTGCGCATGGAAGCTGTGGAGCGGAAT
GTGGGGGTTCATCGTGCGCAGCCGTCCTTGTAACCCTGATTCTCCTGGGAATCTTGGTTTTTGGC
ATCTGGTTTTGCCTATAGCCGAGGCCACTTTGACAGAACAAAGAAAGGGACTTCGAGTAAGAAG
GTGATTTACAGCCAGCCTAGTGCCCGAAGTGAAGGAGAATTCAAACAGACCTCGTCATTCCTG
GT**GTGA**GCCTGGTTCGGCTCACCGCCTATCATCTGCATTTGCCTTACTCAGGTGCTACCGGACT
CTGGCCCCTGATGTCTGTAGTTTTCACAGGATGCCTTATTTGTCTTCTACACCCACAGGGCCC
CCTACTTCTTCGGATGTGTTTTTAATAATGTCAGCTATGTGCCCCATCCTCCTTCATGCCCTC
CCTCCCTTTCTACCACTGCTGAGTGGCCTGGAAGTTGTTTAAAGTGTTTATTCCCCATTTCT
TTGAGGGATCAGGAAGGAATCCTGGGTATGCCATTGACTTCCCTTCTAAGTAGACAGCAAAAA
TGCGGGGGGTGCGAGGAATCTGCACTCAACTGCCACCTGGCTGGCAGGGATCTTTGAATAGG
TATCTTGAGCTTGGTTCTGGGCTCTTTCCTTGTGTACTGACGACCAGGGCCAGCTGTTCTAGA
GCGGGAATTAGAGGCTAGAGCGGCTGAAATGGTTGTTTGGTGATGACACTGGGGTCCTTCCAT
CTCTGGGGCCCACTCTCTTCTGTCTTCCCATGGGAAGTGCCACTGGGATCCCTCTGCCCTGTC
CTCCTGAATACAAGCTGACTGACATTGACTGTGTCTGTGGAAAATGGGAGCTCTTGTTGTGGA
GAGCATAGTAAATTTTCAGAGAACTTGAAGCCAAAAGGATTTAAAACCGCTGCTCTAAAGAAA
AGAAAACCTGGAGGCTGGGCGCAGTGGCTCACGCCTGTAATCCCAGAGGCTGAGGCAGGCGGAT
CACCTGAGGTCGGGAGTTCGGGATCAGCCTGACCAACATGGAGAAACCCTACTGGAAATACAA
AGTTAGCCAGGCATGGTGGTGCATGCCTGTAGTCCCAGCTGCTCAGGAGCCTGGCAACAAGAG
CAAACTCCAGCTCAAAAAAAAAAAAAAAAAA

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FIGURE 366

MGTKAQVERKLLCLFILAILLCSLALGSVTVHSSEPEVRIPENNPVKLS CAYSGFSSPRVEWK
FDQGD TTRLVCYNNKITASYEDRVTF LPTGITFKSVTREDTGTYTCMVSEEGGNSYGEVKVKL
IVLVPPSKPTVNI PSSATIGNRAVLTCSEQDGSP PSEYTWFKDGIVMPTNPKSTRAFSNSSYV
LNPTTGELVFDPLSASDTGEYSCEARNGYGT PMTSNAVRMEAVERNVGVIVA AVLVT LILLGI
LVFGIWFAYS RGHFDRTKKGTSSKKVIYSQPSARSEGEFKQTSSFLV

Important features:**Signal sequence:**

amino acids 1-27

Transmembrane domain:

amino acids 238-255

N-glycosylation site.

amino acids 185-189

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 270-274

Casein kinase II phosphorylation site.amino acids 34-38, 82-86, 100-104, 118-122, 152-156, 154-158,
193-197, 203-207, 287-291**N-myristoylation site.**

amino acids 105-111, 116-122, 158-164, 219-225, 237-243, 256-262

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FIGURE 367

GGGGAGAGGAATTGACCATGTAAAAGGAGACTTTTTTTTTTTGGTGGTGGTGGCTGTTGGGTGCCTTGCAAAAATG
AAGGATGCAGGACGCAGCTTTCTCCTGGAACCGAACGCAATGGATAAACTGATTGTGCAAGAGAGAAGGAAGAAC
GAAGCTTTTTCTTGTGAGCCCTGGATCTTAACACAAATGTGTATATGTGCACACAGGGAGCATTCAAGAATGAAA
TAAACCAGAGTTAGACCCGCGGGGGTTGGTGTGTTCTGACATAAAATAAATAATCTTAAAGCAGCTGTTCCCTCC
CCACCCCCAAAAAAGGATGATTGGAAATGAAGAACCAGGATTCACAAAGAAAAAAGTATGTTCATTTTTCTC
TATAAAGGAGAAAGTGAGCCAAGGAGATATTTTTGGAATGAAAAGTTTGGGGCTTTTTTAGTAAAGTAAAGAACT
GGTGTGGTGGTGTTCCTTTCTTTTTGAATTTCCACAAGAGGAGAGGAAATTAATAATACATCTGCAAAGAAA
TTTCAGAGAAGAAAAGTTGACCGCGGCAGATTGAGGCATTGATTGGGGGAGAGAAACCAGCAGAGCACAGTTGGA
TTTGTGCCTATGTTGACTAAAATTGACGGATAATTGCAGTTGGATTTTTCTTCATCAACCTCCTTTTTTTTAAAT
TTTTATTCTTTTTGGTATCAAGATCATGCGTTTTCTCTTGTCTTAAACCACCTGGATTTCCATCTGGATGTTGCT
GTGATCAGTCTGAAATACAACCTGTTGAATTCAGAAAGGACCAACACCAGATAAATTATGAATGTTGAACAAGAT
GACCTTACATCCACAGCAGATAATGATAGGTCCTAGGTTTAAACAGGGCCCTATTTGACCCCTGCTTGTGGTGCT
GCTGGCTCTTCAACTTCTTGTGGTGGCTGGTCTGGTGGGGCTCAGACCTGCCCTTCTGTGTGCTCCTGCAGCAA
CCAGTTTCAGCAAGGTGATTTGTGTTTCGGAAAAACCTGCGTGAGGTTCCGGATGGCATCTCCACCAACACACGGCT
GCTGAACCTCCATGAGAACCAATCCAGATCATCAAAGTGAACAGCTTCAAGCACTTGAGGCACCTTGGAATCCT
ACAGTTGAGTAGGAACCATATCAGAACCATTGAAATTGGGGCTTTCAATGGTCTGGCGAACCTCAACACTCTGGA
ACTCTTTGACAATCGTCTTACTACCATCCCGAATGGAGCTTTTGTATACTTGTCTAAACTGAAGGAGCTCTGGTT
GCGAAACAACCCCATTGAAAGCATCCCTTCTTATGCTTTTAAACAGAATTCCTTCTTTGCGCCGACTAGACTTAGG
GGAATTGAAAAGACTTTTCATACATCTCAGAAGGTGCCTTTGAAGGTCTGTCCAACCTGAGGTATTTGAACCTTGC
CATGTGCAACCTTCGGGAAATCCCTAACCTCACACCGCTCATAAAACTAGATGAGCTGGATCTTTCTGGGAATCA
TTTATCTGCCATCAGGCCTGGCTCTTTCAGGGTTTGATGCACCTTCAAAAACTGTGGATGATACAGTCCCAGAT
TCAAGTGATTGAACGGAATGCCTTTGACAACCTTCAGTCACTAGTGAGATCAACCTGGCACACAATAATCTAAC
ATTACTGCCTCATGACCTCTTCACTCCCTTGATCATCTAGAGCGGATACATTTACATCACAACCCTTGGAACCTG
TAAGTGACATACTGTGGCTCAGCTGGTGGATAAAAGACATGGCCCCCTCGAACACAGCTTGTGTGCCCCGGTG
TAACACTCCTCCCAATCTAAAGGGGAGGTACATTGGAGAGCTCGACCAGAATTACTTCACATGCTATGCTCCGGT
GATTGTGGAGCCCCCTGCAGACCTCAATGTCACTGAAGGCATGGCAGCTGAGCTGAAATGTGCGGCCCTCCACATC
CCTGACATCTGTATCTTGGATTACTCCAAATGGAACAGTCATGACACATGGGGCGTACAAAGTGCGGATAGCTGT
GCTCAGTGATGGTACGTTAAATTTACAAATGTAAGTGTGCAAGATACAGGCATGTACACATGTATGGTGAGTAA
TTCCGTTGGGAATACTACTGCTTCAGCCACCCTGAATGTTACTGCAGCAACCCTACTCCTTTCTCTTACTTTTC
AACCCTCACAGTAGAGACTATGGAACCGTCTCAGGATGAGGCACGGACCACAGATAACAATGTGGGTCCCCTCC
AGTGGTGCAGTGGGAGACCACCAATGTGACCACCTCTCTCACACCACAGAGCACAAGGTGCAGAGAGAAAACCTT
CACCATCCCAGTGACTGATATAAACAGTGGGATCCCAGGAATTGATGAGGTCATGAAGACTACCAAAATCATCAT
TGGGTGTTTTGTGGCCATCACACTCATGGCTGCAGTGATGCTGGTCATTTTCTACAAGATGAGGAAGCAGCACCA
TCGGCAAAACCATCACGCCCCAACAAAGGACTGTTGAAATTATTAATGTGGATGATGAGATTACGGGAGACACACC
CATGGAAGCCACCTGCCCATGCCTGCTATCGAGCATGAGCACCTAAATCACTATAACTCATACAAATCTCCCTT
CAACCACACAACAACAGTTAACACAATAAATTCATACACAGTTCAGTGCATGAACCGTTATTGATCCGAATGAA
CTCTAAAGACAATGTACAAGAGACTCAAATCTAAACATTTACAGAGTTACAAAAACAAACAATCAAAAAAAAA
GACAGTTTATTAAAAATGACACAAATGACTGGGCTAAATCTACTGTTTCAAAAAAGTGTCTTTACAAAAAACAA
AAAAGAAAAGAAATTTATTTATTAAAAATTCATTGTGATCTAAAGCAGACAAAAA

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FIGURE 368

MLNKMTLHPQQIMIGPRFNRALFDPLLVLALLQLLVVAGLVRAQTCPSVCSCSNQFSKVICVRKNLREVPDGIS
TNTRLLNLHENQIQI IKVNSFKHLRHLEILQLSRNHIRTIEIGAFNGLANLNTLELFDNRLTTIPNGAFVYLSKL
KELWLRNNPIESIPSYAFNRIPSLRRLDLGELKRLSYISEGAFEGLSNRLRYLNLAMCNLREIPNLTPLIKLDELD
LSGNHLSAIRPGSFQGLMHLQKLWMIQSQIQVIERNAFDNLQSLVEINLAHNNLTLLPHDLFTPLHHLERIHLHH
NPWNCNCIDILWLSWWIKDAPSNNTACCARCNTPPNLKGRYIGELDQNYFTCYAPVIVEPPADLNVTEGMAAELKC
RASTSLTSVSWITPNGTVMTHGAYKVRIAVLSDGTNLFTNVTVQDTCMYTCMVNSVGNNTASATLNVTAATTP
FSYFSTVTVETMEPSQDEARTDNNVGPTPVVDWETTNVTTSLTPQSTRSTEKFTIPVTDINSGIPGIDEVMKT
TKIIIGCFVAITLMAAVMLVIFYKMRQHRQNHAPTRTVEI INVDEITGDTPMESHLPMPAIEHEHLNHYS
YKSPFNHTTTVNTINSIHSSVHEPLLIRMNSKDNVQETQI

Important features:**Signal sequence:**

amino acids 1-44

Transmembrane domain:

amino acids 523-543

N-glycosylation site.amino acids 278-282, 364-368, 390-394, 412-416, 415-419, 434-438, 442-446,
488-492, 606-610**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 183-187

Casein kinase II phosphorylation site.

amino acids 268-272, 417-421, 465-469, 579-583, 620-624

N-myristoylation site.amino acids 40-46, 73-79, 118-124, 191-197, 228-234, 237-243, 391-397,
422-428, 433-439, 531-537

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FIGURE 369

CAAAACTTGCCTCGCGGAGAGCGCCAGCTTGACTTGAATGGAAGGAGCCCCGAGCCCCGCGGAGCGCAGCTGAGAC
TGGGGGAGCGCGTTTCGGCCTGTGGGGCGCCGCTCGGCGCCGGGGCGCAGCAGGGAAGGGGAAGCTGTGGTCTGCC
CTGCTCCACGAGGCGCCACTGGTGTGAACCGGGAGAGCCCCCTGGGTGGTCCCGTCCCCTATCCCTCCTTTATATA
GAAACCTTCCACACTGGGAAGGCAGCGGCGAGGCAGGAGGGCTCATGGTGAAGGAGGCGGGCTGATCTGCAG
GCGCACAGCATTCAGATTTACAGATTTTACAGATACCAATGGGAAGGCGAGGAGGCAGAACAGCCTGCCTGGT
TCCATCAGCCCCGGCGCCAGGCGCATCTGACTCGGCACCCCCCTGCAGGCACCATGGCCCAGAGCCGGGTGCTGC
TGCTCCTGCTGCTGCTGCCGCCACAGCTGCACCTGGGACCTGTGCTTGCCGTGAGGGCCCCAGGATTTGGCCGAA
GTGGCGGCCACAGCCTGAGCCCCGAAGAGAACGAATTTGCGGAGGAGGAGCCGGTGCTGGTACTGAGCCCCGAGG
AGCCCCGGGCCTGGCCCAGCCGCGGTGAGCTGCCCCCGAGACTGTGCCTGTTCCAGGAGGGCGTGGTGGACTGTG
GCGGTATTGACCTGCGTGAGTTCGCGGGGACCTGCCTGAGCACACCAACCACCTATCTCTGCAGAACCAACCAGC
TGGAAAAGATCTACCCTGAGGAGCTCTCCCGGCTGCACCGGCTGGAGACACTGAACCTGCAAAAACAACCGCCTGA
CTTCCCGAGGGCTCCCAGAGAAGGCGTTTGAGCATCTGACCAACCTCAATTACCTGTACTTTGGCCAATAACAAGC
TGACCTTGGCACCCCCGCTTCCTGCCAAACGCCCTGATCAGTGTGGACTTTGCTGCCAACTATCTCACCAGATCT
ATGGGCTCACCTTTTGGCCAGAAGCCAACTTGAGGTCTGTGTACCTGCACAACAACAAGCTGGCAGACGCCGGGC
TGCCCGGACAACATGTTCAACGGCTCCAGCAACGTGAGGTCTCATCCTGTCCAGCAACTTCTGCGCCACGTGC
CCAAGCACCTGCCGCTGCCCTGTACAAGCTGCACCTCAAGAACAACAAGCTGGAGAAGATCCCCCGGGGGCCT
TCAGCGAGCTGAGCAGCCTGCGCGAGCTATACCTGCAGAACAACTACCTGACTGACGAGGGCCTGGACAACGAGA
CCTTCTGGAAGCTCTCCAGCCTGGAGTACCTGGATCTGTCCAGCAACAACCTGTCTCGGGTCCCAGCTGGGCTGC
CGCGCAGCCTGGTGTGCTGCACTTGAGAGAAGAACGCCATCCGGAGCGTGGACGCGAATGTGCTGACCCCCATCC
GCAGCCTGGAGTACCTGCTGCTGCACAGCAACCAGCTGCGGGAGCAGGGCATCCACCCACTGGCCTTCCAGGGCC
TCAAGCGGTTGCACACGGTGCACCTGTACAACAACGCGCTGGAGCGCGTGCCAGTGGCCTGCCTCGCCGCGTGC
GCACCCCTCATGATCCTGCACAACCAGATCACAGGCATTTGGCCGCGAAGACTTTGCCACCACCTACTTCTGGAGG
AGCTCAACCTCAGCTACAACCGCATCACCAGCCCACAGGTGCACCGCGACGCTTCCGCAAGCTGCGCCTGCTGC
GCTCGCTGGACCTGTGCGGCAACCGGCTGCACACGCTGCCACCTGGGCTGCCTCGAAATGTCCATGTGCTGAAGG
TCAAGCGCAATGAGCTGGCTGCCTTGGCACGAGGGGCGCTGGCGGGCATGGCTCAGCTGCGTGAGCTGTACCTCA
CCAGCAACCGACTGCGCAGCCGAGCCCTGGGCCCCCGTGCTGGGTGGACCTCGCCCATCTGCAGCTGCTGGACA
TCGCGGGGAATCAGCTCACAGAGATCCCCGAGGGGCTCCCCGAGTCACTTGAGTACCTGTACCTGCAGAACAAACA
AGATTAGTGCGGTGCCCCGCAATGCCTTCGACTCCACGCCCAACCTCAAGGGGATCTTTCTCAGGTTTAACAAGC
TGGCTGTGGGCTCCGTGGTGGACAGTGCCTTCCGGAGGCTGAAGCACCTGCAGGTCTTGACATTGAAGGCAACT
TAGAGTTTGGTGACATTTCCAAGGACCGTGGCCGCTTGGGGAAGGAAAAGGAGGAGGAGGAAGAGGAGGAGGAGG
AGGAAGAGGAAACAAGATAGTGACAAGGTGATGCAGATGTGACCTAGGATGATGGACCGCCGGACTCTTTTCTGC
AGCACACGCTGTGTGCTGTGAGCCCCCCTGCTGCCGTGCTCACACAGACACACCCAGCTGCACACATGAGGCA
TCCACATGACACGGGCTGACACAGTCTCATATCCCCACCCCTTCCCACGGCGTGTCCCACGGCCAGACACATGC
ACACACATCACACCCCTCAAACACCCAGCTCAGCCACACACAACCTACCCTCCAAACCACACAGTCTCTGTACAC
CCCCACTACCGCTGCCACGCCCTCTGAATCATGCAGGGAAGGGTCTGCCCCCTGCCCTGGCACACACAGGCACCCA
TTCCCTCCCCCTGCTGACATGTGTATGCGTATGCATACACACCACACACACACATGCACAAGTCATGTGCGAA
CAGCCCTCCAAAGCCTATGCCACAGACAGCTCTTGCCCCAGCCAGAATCAGCCATAGCAGCTCGCCGTCTGCCCT
GTCCATCTGTCCGTCCGTTCCTGGAGAAGACACAAGGGTATCCATGCTCTGTGGCCAGGTGCCTGCCACCCTCT
GGAACCTACAAAAGCTGGCTTTTATTCCTTTCCCATCCTATGGGGACAGGAGCCTTCAGGACTGCTGGCCTGGCC
TGGCCACCCCTGCTCCTCCAGGTGCTGGGCAGTCACTCTGCTAAGAGTCCCTCCCTGCCACGCCCTGGCAGGACA
CAGGCACTTTTCCAATGGGCAAGCCCAGTGGAGGCAGGATGGGAGAGCCCCCTGGGTGCTGCTGGGGCCTTGGGG
CAGGAGTGAAGCAGAGGTGATGGGGCTGGGCTGAGCCAGGGAGGAAGGCCAGCTGCACCTAGGAGACACCTTT
GTTCTTCAGGCCTGTGGGGGAAGTCCGGGTGCCTTTATTTTATTTCTTTCTAAGGAAAAAAATGATAAAAT
CTCAAAGCTGATTTTCTTGTATAGAAAACTAATATAAAAGCATTATCCCTATCCCTGCAAAAAA

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FIGURE 370

MEGEEAEQPAWFHQWRPGASDSAPPAGTMAQSRVLLLLLLLLPPQLHLGPVLAVRAPGFGRSG
GHSLSPEENEFAEEEPVLVLSPEEPGPGPAAVSCPRDCACSQEGVVD CGGIDLREFPGDLPEH
TNHLSLQNNQLEKIYPEELSRLEHRLTLNLQNNRLTSRGLPEKAFEHLTNLNYLYLANNKLT
APRFLPNALISVDFAANYLTKIYGLTFGQKPNLRSVYLHNNKLADAGLPDNMFNGSSNVEVLI
LSSNFLRHVPKHLPPALYKLHLKNNKLEKIIPGAFSELSSLRELYLQNNYLTDEGLDNETFWK
LSSLEYLDLSSNNLSRVPAGLPRSLVLLHLEKNAIRSVDANVLTPIRSLEYLLLHSNQLREQG
IHPLAFQGLKRLHTVHLYNNALERVPSGLPRRVRTLMLHNQITGIGREDFATTYFLEELNLS
YNRITSPQVHRDAFRKLRLRLSLDLSGNRLHTLPPGLPRNVHVLKVKRNELAAALARGALAGMA
QLRELYLTSNRLRSRALGPRAWVDLAHLQLLDIAGNQLTEIPEGLPESLEYLYLQNNKISAVP
ANAFDSTPNLKGIFLRFNKLAVGSVVD SAFRRLKHLQVLDIEGNLEFGDISKDRGRLGKEKEE
EEEEEEEEEEETR

Important features:**Signal sequence:**

amino acids 1-48

N-glycosylation site.

amino acids 243-247, 310-314, 328-332, 439-443

Casein kinase II phosphorylation site.

amino acids 68-72, 84-88, 246-250, 292-296, 317-321, 591-595

N-myristoylation site.amino acids 19-25, 107-113, 213-219, 217-223, 236-242, 335-341,
477-483, 498-502, 539-545, 548-554**Leucine zipper pattern.**amino acids 116-138, 251-273, 258-280, 322-344, 464-486, 471-493,
535-557

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FIGURE 371

CACTTTCTCCCTCTCTTCTTTACTTTTCGAGAAACCGCGCTTCCGCTTCTGGTTCGAGAGACCTCGGAGACCGCG
CCGGGAGACGGAGGTGCTGTGGGTGGGGGGGACCTGTGGCTGCTCGTACCGCCCCCACCCTCCTCTTCTGCAC
TGCCGTCCTCCGGAAGACCTTTTCCCCTGCTCTGTTTCTTACCAGAGTCTGTGCATCGCCCCGGACCTGGCCGG
GAGGAGGCTTGGCCGGCGGGAGATGCTCTAGGGGCGGCGGGAGGAGCGGCCGGCGGGACGGAGGGCCCGGCAG
GAAGATGGGCTCCCGTGGACAGGGACTCTTGCTGGCGTACTGCCTGCTCCTTGCCTTTGCCTCTGGCCTGGTCCT
GAGTCGTGTGCCCCATGTCCAGGGGGAACAGCAGGAGTGGGAGGGGACTGAGGAGCTGCCGTCGCCTCCGGACCA
TGCCGAGAGGGCTGAAGAACAACATGAAAAATACAGGCCAGTCAGGACCAGGGGCTCCCTGCTTCCCGGTGCTT
GCGCTGCTGTGACCCCGGTACCTCCATGTACCCGGCGACCGCCGTGCCCCAGATCAACATCACTATCTTGAAAGG
GGAGAAGGGTGACCGCGGAGATCGAGGCCTCCAAGGGAAATATGGCAAACAGGCTCAGCAGGGGCCAGGGGCCA
CACTGGACCCAAAGGGCAGAAGGGCTCCATGGGGGCCCTGGGGAGCGGTGCAAGAGCCACTACGCCGCTTTTC
GGTGGGCCGGAAGAAGCCCATGCACAGCAACCACTACTACCAGACGGTGATCTTCGACACGGAGTTCGTGAACCT
CTACGACCACTTCAACATGTTACCGGCAAGTTCTACTGCTACGTGCCCGGCCCTCTACTTCTTCAGCCTCAACGT
GCACACCTGGAACCAGAAGGAGACCTACCTGCACATCATGAAGAACGAGGAGGAGGTGGTGATCTTGTTCGCGCA
GGTGGGCGACCGCAGCATCATGCAAAGCCAGAGCCTGATGCTGGAGCTGCGAGAGCAGGACCAGGTGTGGGTACG
CCTCTACAAGGGCGAACGTGAGAACGCCATCTTCAGCGAGGAGCTGGACACCTACATCACTTCAGTGGCTACCT
GGTCAAGCACGCCACCGAGCCCTTAGCTGGCCGGCCACCTCCTTCTCTCGCCACCTTCCACCCCTGCGCTGTGC
TGACCCACCGCCTCTTCCCCGATCCCTGGACTCCGACTCCCTGGCTTTGGCATTTCAGTGAGACGCCCTGCACAC
ACAGAAAGCCAAAGCGATCGGTGCTCCCAGATCCCGCAGCCTCTGGAGAGAGCTGACGGCAGATGAAATCACCAG
GGCGGGGACCCCGGAGAACCTCTGGGACCTTCCGCGGCCCTCTCTGCACACATCCTCAAGTGACCCCGCACGG
CGAGACGCGGGTGCGCGGAGGGCGTCCCAGGGTGCGGCACCGCGGCTCCAGTCTTGGAATAATTAGGCAAATT
CTAAAGGTCTCAAAAGGAGCAAAGTAAACCGTGGAGGACAAAGAAAAGGGTTGTTATTTTTGTCTTTCCAGCCAG
CCTGCTGGCTCCCAAGAGAGAGGCCTTTTTCAGTTGAGACTCTGCTTAAGAGAAGATCCAAAGTTAAAGCTCTGGG
GTCAGGGGAGGGGCCGGGGGAGGAACTACCTCTGGCTTAATTCTTTTAAGCCACGTAGGAACCTTTCTTGAGGG
ATAGGTGGACCTTGACATCCCTGTGGCCTTGCCCCAAGGGCTCTGCTGGTCTTTCTGAGTCACAGCTGCGAGGTGA
TGGGGGCTGGGGCCCCAGGCGTCAGCCTCCCAGAGGGACAGCTGAGCCCCCTGCCTTGGCTCCAGGTTGGTAGAA
GCAGCCGAAGGGCTCCTGACAGTGGCCAGGACCCCTGGGTCCCCAGGCCTGCAGATGTTTCTATGAGGGGCAG
AGCTCCTTGGTACATCCATGTGTGGCTCTGCTCCACCCCTGTGCCACCCAGAGCCCTGGGGGGTGGTCTCCATG
CCTGCCACCCCTGGCATCGGCTTTCTGTGCCGCTCCCACACAAATCAGCCCCAGAAGGCCCCGGGGCCTTGGCTT
CTGTTTTTTTATAAAACACCTCAAGCAGCACTGCAGTCTCCCATCTCCTCGTGGGCTAAGCATCACCGCTTCCACG
TGTGTTGTGTTGGTTGGCAGCAAGGCTGATCCAGACCCCTTCTGCCCCACTGCCCTCATCCAGGCCTCTGACCA
GTAGCCTGAGAGGGGCTTTTCTAGGCTTCAGAGCAGGGGAGAGCTGGAAGGGGCTAGAAAGCTCCCGCTTGTCT
GTTTCTCAGGCTCCTGTGAGCCTCAGTCCTGAGACCAGAGTCAAGAGGAAGTACACGTCCCAATCACCCGTGTCA
GGATTCACTCTCAGGAGCTGGGTGGCAGGAGAGGCAATAGCCCCCTGTGGCAATTGCAGGACCAGCTGGAGCAGGG
TTGCGGTGTCTCCACGGTGCTCTCGCCCTGCCCATGGCCACCCAGACTCTGATCTCCAGGAACCCCATAGCCCC
TCTCCACCTCACCCCATGTTGATGCCCAGGGTCACTCTTGCTACCCGCTGGGCCCCCAAACCCCGCTGCCTCTC
TTCCTTCCCCCATCCCCACCTGGTTTTGACTAATCCTGCTTCCCTCTCTGGGCCTGGCTGCCGGGATCTGGGG
TCCCTAAGTCCCTCTCTTTAAAGAACTTCTGCGGGTCAGACTCTGAAGCCGAGTTGCTGTGGGCGTGCCCGGAAG
CAGAGCGCCACACTCGCTGCTTAAGCTCCCCAGCTCTTTCAGAAAACATTAAACTCAGAATTGTGTTTTCAA

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FIGURE 372

MGSRGQGGLLLAYCLLLAFASGLVLSRVPHVQGEQQEWEGTEELPSPPDHAERAEQHEKYRPS
QDQGLPASRCLRCCDPGTSMPATAVPQINITILKGEKGDRGDRGLQGKYGKTGSAGARGHTG
PKGQKGSMSGAPGERCKSHYAAFSVGRKKPMHSNHYYQTVIFDTEFVNLYDHFNMFTGKFYCYV
PGLYFFSLNVHTWNQKETYLHIMKNEEEVVILFAQVGDRSIMQSQSLMLELREQDQVWVRLYK
GERENAI FSEELDTYITFSGYLVKHATEP

Important features:**Signal sequence.**

amino acids 1-25

N-glycosylation site.

amino acids 93-97

N-myristoylation sites.

amino acids 7-13, 21-27, 67-73, 117-123, 129-135

Amidation site.

amino acids 150-154

Cell attachment sequence.

amino acids 104-107

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FIGURE 373

CGGAGTGGTGCGCCAACGTGAGAGGAAACCCGTGCGCGGCTGCGCTTTCCTGTCCCCAAGCCG
TTCTAGACGCGGGAAAA**ATG**CTTTCTGAAAGCAGCTCCTTTTTGAAGGGTGTGATGCTTGGAA
GCATTTTCTGTGCTTTGATCACTATGCTAGGACACATTAGGATTGGTCATGGAAATAGAATGC
ACCACCATGAGCATCATCACCTACAAGCTCCTAACAAAGAAGATATCTTGAAAATTTTCAGAGG
ATGAGCGCATGGAGCTCAGTAAGAGCTTTCGAGTATACTGTATTATCCTTGTAACCCCAAAG
ATGTGAGTCTTTGGGCTGCAGTAAAGGAGACTTGGACCAAACACTGTGACAAAGCAGAGTTCT
TCAGTTCTGAAAATGTTAAAGTGTTTGAGTCAATTAATATGGACACAAATGACATGTGGTTAA
TGATGAGAAAAGCTTACAAATACGCCTTTGATAAGTATAGAGACCAATACAACCTGGTTCTTCC
TTGCACGCCCCACTACGTTTGCTATCATTGAAAACCTAAAGTATTTTTTGTAAAAAAGGATC
CATCACAGCCTTTCTATCTAGGCCACACTATAAAATCTGGAGACCTTGAATATGTGGGTATGG
AAGGAGGAATTGTCTTAAGTGTAGAATCAATGAAAAGACTTAACAGCCTTCTCAATATCCCAG
AAAAGTGTCCTGAACAGGGAGGGATGATTTGGAAGATATCTGAAGATAAACAGCTAGCAGTTT
GCCTGAAATATGCTGGAGTATTTGCAGAAAATGCAGAAGATGCTGATGGAAAAGATGTATTTA
ATACCAAATCTGTTGGGCTTTCTATTAAAGAGGCAATGACTTATCACCCCAACCAGGTAGTAG
AAGGCTGTTGTTTCAGATATGGCTGTACTTTTAATGGACTGACTCCAAATCAGATGCATGTGA
TGATGTATGGGGTATACCGCCTTAGGGCATTGGGCATATTTCAATGATGCATTGGTTTTCT
TACCTCCAAATGGTTCTGACAATGAC**TGA**GAAAGTGGTAGAAAAGCGTGAATATGATCTTTGTA
TAGGACGTGTGTTGTCATTATTTGTAGTAGTAACTACATATCCAATACAGCTGTATGTTTCTT
TTTCTTTTCTAATTTGGTGGCACTGGTATAACCACACATTAAAGTCAGTAGTACATTTTTAAA
TGAGGGTGGTTTTTTTCTTTAAACACATGAACATTGTAAATGTGTTGGAAAGAAGTGTTTTA
AGAATAATAATTTTGCAAATAAACTATTAATAAATATTATATGTGATAAATTCTAAATTATGA
ACATTAGAAATCTGTGGGGCACATATTTTTGCTGATTGGTTAAAAAATTTTAACAGGTCTTTA
GCGTTCTAAGATATGCAAATGATATCTCTAGTTGTGAATTTGTGATTAAAGTAAAACCTTTTAG
CTGTGTGTTCCCTTTACTTCTAATACTGATTTATGTTCTAAGCCTCCCCAAGTTCCAATGGAT
TTGCCTTCTCAAATGTACAACCTAAGCAACTAAAGAAAATTAAGTGAAAGTTGAAAAAT

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FIGURE 374

MLSESSSFLKGVMLGSIFCALITMLGHIRIGHGNRMHHHEHHHLQAPNKEDILKISEDERMELSKSFRVYCIILV
KPKDVSLWAAVKETWTKHCDKAEFFSSSENVKVFESINMDTNDMWLMMRKAYKYAFDKYRDQYNWFFLARPTTFAI
IENLKYFLLKKDPSQPFYLGHTIKSGDLEYVGMEGGIVLSVESMKRLNSLLNIPEKCPEQGGMIWKISEDKQLAV
CLKYAGVFAENAEDADGKDVFNKTSVGLS IKEAMTYHPNQVVEGCCSDMAVTFNGLTPNQMHVMMYGVYRLRAFG
HIFNDALVFLPPNGSDND

Important features:**Signal sequence:**

amino acids 1-33

N-glycosylation site.

amino acids 121-125, 342-346

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 319-323, 464-468

Casein kinase II phosphorylation site.amino acids 64-132, 150-154, 322-326, 331-335, 368-372, 385-389, 399-403,
409-413, 473-477, 729-733, 748-752**Tyrosine kinase phosphorylation site.**

amino acids 736-743

N-myristoylation site.amino acids 19-25, 23-29, 136-142, 397-403, 441-447, 544-550, 558-564,
651-657, 657-663, 672-672**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 14-25

Cell attachment sequence.

amino acids 247-250

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FIGURE 375

GTTGTGTCCTTCAGCAAAACAGTGGATT TAAATCTCCTTGCACAAGCTTGAGAGCAACACAAT
CTATCAGGAAAGAAAGAAAGAAAAAACCGAACCTGACAAAAAAGAAGAAAAAGAAGAAA
AAAAATCATGAAAACCATCCAGCCAAAATGCACAATTCTATCTCTTGGGCAATCTTCACGGG
GCTGGCTGCTCTGTGTCTCTTCCAAGGAGTGCCCGTGCGCAGCGGAGATGCCACCTTCCCCAA
AGCTATGGACAACGTGACGGTCCGGCAGGGGGAGAGCGCCACCCTCAGGTGCACTATTGACAA
CCGGGTCACCCGGGTGGCCTGGCTAAACCGCAGCACCATCCTCTATGCTGGGAATGACAAGTG
GTGCCTGGATCCTCGCGTGGTCCTTCTGAGCAACACCCAAACGCAGTACAGCATCGAGATCCA
GAACGTGGATGTGTATGACGAGGGCCCTTACACCTGCTCGGTGCAGACAGACAACCAACCCAAA
GACCTCTAGGGTCCACCTCATTTGTGCAAGTATCTCCCAAATTTGTAGAGATTTCTTCAGATAT
CTCCATTAATGAAGGGAACAATATTAGCCTCACCTGCATAGCAACTGGTAGACCAGAGCCTAC
GGTTACTTGAGACACATCTCTCCCAAAGCGGTTGGCTTTGTGAGTGAAGACGAATACTTGGA
AATTCAGGGCATCACCCGGGAGCAGTCAGGGGACTACGAGTGCAGTGCCTCCAATGACGTGGC
CGCGCCCGTGGTACGGAGAGTAAAGGTCACCGTGAAC TATCCACCATACATTTTCAGAAGCCAA
GGGTACAGGTGTCCCCGTGGGACAAAAGGGGACACTGCAGTGTGAAGCCTCAGCAGTCCCCTC
AGCAGAATTCCAGTGGTACAAGGATGACAAAAGACTGATTGAAGGAAAGAAAGGGGTGAAAGT
GGAAAACAGACCTTTCTCTCAAACTCATCTTCTTCAATGTCTCTGAACATGACTATGGGAA
CTACACTTGCGTGGCCTCCAACAAGCTGGGCCACACCAATGCCAGCATCATGCTATTTGGTCC
AGGCGCCGTCAGCGAGGTGAGCAACGGCACGTCGAGGAGGGCAGGCTGCGTCTGGCTGCTGCC
TCTTCTGGTCTTGACCTGCTTCTCAAATTTTGATGTGAGTGCCACTTCCCCACCCGGGAAAG
GCTGCCGCCACCACCACCAACACAACAGCAATGGCAACACCGACAGCAACCAATCAGATA
TATACAAATGAAATTAGAAGAAACACAGCCTCATGGGACAGAAATTTGAGGGAGGGGAACAAA
GAATACTTTGGGGGGAAAAGAGTTTTAAAAAAGAAATTGAAAATTGCCTTGCAGATATTTAGG
TACAATGGAGTTTTCTTTTCCCAAACGGGAAGAACACAGCACACCCGGCTTGGACCCACTGCA
AGCTGCATCGTGCAACCTCTTTGGTGCCAGTGTGGGCAAGGGCTCAGCCTCTCTGCCCACAGA
GTGCCCCCACGTGGAACATTCTGGAGCTGGCCATCCCAAATTC AATCAGTCCATAGAGACGAA
CAGAATGAGACCTTCCGGCCCAAGCGTGGCGCTGCGGGCACTTTGGTAGACTGTGCCACCACG
CGGTGTGTTGTGAAACGTGAAATAAAAAGAGCAAAAAAAA

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FIGURE 376

MKTIQPKMHNSISWAI FTGLAALCLFQGV PVRSGDATFPKAMD NVTVRQGESATLRCTIDNRV
TRVAWLNRSTILYAGNDKWCLDPRVLLSNTQTQYSIEIQNV DVYDEGPYTCSVQTDNHPKTS
RVHLIVQVSPKIVEISSDISINEGNNISLTCIATGRPEPTVTWRHISPKAVGFVSEDEYLEIQ
GITREQSGDYEC SASNDVAAPV VRRVKVTVNYPPYISEAKGTGVPVGQKGT LQCEASAVPSAE
FQWYKDDKRLIEGKKGVKVENRPFLSKLIFFNVSEHDYGN YTCVASNKLGHTNASIMLFGPGA
VSEVSNGTSRRAGCVWLLPLLVLHLLK F

Important features:**Signal peptide:**

amino acids 1-28

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FIGURE 377

CTTCTTTGAAAAGGATTATCACCTGATCAGGTTCTCTCTGCATTTGCCCCCTTTAGATTGTGAA
ATGTGGCTCAAGGTCTTCACAACTTTCCCTTTCCCTTTGCAACAGGTGCTTGCTCGGGGCTGAAG
GTGACAGTGCCATCACACACTGTCCATGGCGTCAGAGGTCAGGCCCTCTACCTACCCGTCCAC
TATGGCTTCCACACTCCAGCATCAGACATCCAGATCATATGGCTATTTGAGAGACCCACACA
ATGCCCAAATACTTACTGGGCTCTGTGAATAAGTCTGTGGTTCCTGACTTGGAATACCAACAC
AAGTTCACCATGATGCCACCCAATGCATCTCTGCTTATCAACCCACTGCAGTTCCTTGATGAA
GGCAATTACATCGTGAAGGTCAACATTCAGGGAAATGGAACCTCTATCTGCCAGTCAGAAGATA
CAAGTCACGGTTGATGATCCTGTCAAAAGCCAGTGGTGCAGATTCATCCTCCCTCTGGGGCT
GTGGAGTATGTGGGGAACATGACCCTGACATGCCATGTGGAAGGGGGCACTCGGCTAGCTTAC
CAATGGCTAAAAAATGGGAGACCTGTCCACACCAGCTCCACCTACTCCTTTTCTCCCCAAAC
AATACCCTTCATATTGCTCCAGTAACCAAGGAAGACATTGGGAATTACAGCTGCCTGGTGAGG
AACCCTGTCAGTGAAATGGAAAGTGATATCATTATGCCCATCATATATTATGGACCTTATGGA
CTTCAAGTGAATTCTGATAAAGGGCTAAAAGTAGGGGAAGTGTTTACTGTTGACCTTGGAGAG
GCCATCCTATTTGATTGTTCTGCTGATTCTCATCCCCCAACACCTACTCCTGGATTAGGAGG
ACTGACAATACTACATATATCATTAAAGCATGGGCCTCGCTTAGAAGTTGCATCTGAGAAAGTA
GCCCAGAAGACAATGGACTATGTGTGCTGTGCTTACAACAACATAACCGGCAGGCAAGATGAA
ACTCATTTTCACAGTTATCATCACTTCCGTAGGACTGGAGAAGCTTGCACAGAAAGGAAAATCA
TTGTCACCTTTAGCAAGTATAACTGGAATATCACTATTTTTGATTATATCCATGTGTCTTCTC
TTCCTATGGAAAAAATATCAACCCTACAAAGTTATAAAACAGAACTAGAAGGCAGGCCAGAA
ACAGAATACAGGAAAGCTCAAACATTTTCAGGCCATGAAGATGCTCTGGATGACTTCGGAATA
TATGAATTTGTTGCTTTTCCAGATGTTTCTGGTGTTTCCAGGATTCCAAGCAGGTCTGTTCCA
GCCTCTGATTGTGTATCGGGGCAAGATTTGCACAGTACAGTGTATGAAGTTATTCAGCACATC
CCTGCCCAGCAGCAAGACCATCCAGAG**TGA**ACTTTTCATGGGCTAAACAGTACATTCGAGTGAA
ATTCTGAAGAAACATTTTAAAGGAAAAACAGTGGAAGTATATTAATCTGGAATCAGTGAAGA
AACCAGGACCAACACCTCTTACTCATTATTCCTTTACATGCAGAATAGAGGCATTTATGCAAA
TTGAACTGCAGGTTTTTTCAGCATATACACAATGTCTTGTGCAACAGAAAAACATGTTGGGGAA
ATATTCCTCAGTGGAGAGTCGTTCTCATGCTGACGGGGAGAACGAAAGTGACAGGGGTTTCCT
CATAAGTTTTGTATGAAATATCTCTACAAACCTCAATTAGTTCTACTCTACACTTTCATATC
ATCAACACTGAGACTATCCTGTCTCACCTACAAATGTGGAACTTTACATTGTTTCGATTTTTT
AGCAGACTTTGTTTTATTAAATTTTTATTAGTGTTAAGAATGCTAAATTTATGTTTCAATTTT
ATTTCCAAATTTCTATCTTGTTATTTGTACAACAAAGTAATAAGGATGGTTGTCACAAAAACA
AACTATGCCTTCTCTTTTTTTTCAATCACCAGTAGTATTTTTGAGAAGACTTGTGAACACTT
AAGGAAATGACTATTAAAGTCTTATTTTTTATTTTTTCAAGGAAAGATGGATTCAAATAAATT
ATTCTGTTTTTGCTTTTAAAAA

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FIGURE 378

MWLKVFTTFLSFATGACSGLKVTVPSTVHGVRGQALYLPVHYGFHTPASDIQIIWLFERPHTMPKYLLGSVNKS
VVPDLEYQHKFTMMPPNASLLINPLQFPDEGNYIVKVNIQGNGLSASQKIQVTVDDPVTKPVVQIHPPSGAVEY
VGNMTLTCHVEGGTRLAYQWLKNGRPVHTSSTYSFSPQNNTLHIAPVTKEDIGNYSCLVRNPVSEMESDIIMPII
YYGPYGLQVNSDKGLKVGEVFTVDLGEAILFDCSADSHPPNTYSWIRRTDNTTYIIKHGPRLEVASEKVAQKTMD
YVCCAYNNITGRQDETHFTVIITSVGLEKLAQKGKSLSPASITGISLFLIISMCLLFLWKKYQPYKVIKQKLEG
RPETEYRKAQTFSGHEDALDDFGIYEFVAFPDVSGVSRIPSRVSPASDCVSGQDLHSTVYEVIQHIPAQQQDHPE

Important features:**Signal sequence:**

amino acids 1-18

Transmembrane domain:

amino acids 341-359

N-glycosylation site.

amino acids 73-77, 92-96, 117-121, 153-157, 189-193, 204-208, 276-280, 308-312

Casein kinase II phosphorylation site.

amino acids 129-133, 198-202, 214-218, 388-392, 426-430, 433-437

Tyrosine kinase phosphorylation site.

amino acids 272-280

N-myristoylation site.

amino acids 15-21, 19-25, 118-124, 163-167, 203-209, 231-237, 239-245

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 7-18

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FIGURE 379

ATAGTAGAAGAATGTCTCTGAAATTACTGGATGAGTTTCAGTCATACTTTCACATGGGCACAA
TTTCACATTCAAGCTCCTTATCCTAGGCTAATTTTATATTATGTTAAATCACTTGTTTTTGT
CTCACGGCTTCCTGCCTGCTATAGGCATAATTACGAGGAAGCAGAACTTCTCCAGAAGCAAGC
GCACATGCGTTCCAAAATAAGAGCAAATTCGCTCTAAACACAGGAAAAGACCTGAAGCTTTAA
TTAAGGGGTTACATCCAACCCCAGAGCGCTTTTGTGGGCACTGATTGCTCCAGCTTCTGCGTC
ACTGCGCGAGGGAAGAGGGAAGAGGATCCAGGCGTTAGAC**ATG**TATAGACACAAAAACAGCTG
GAGATTGGGCTTAAAATACCCACCAAGCTCCAAAGAAGAGACCCAAGTCCCCAAAACATTGAT
TTCAGGGCTGCCAGGAAGGAAGAGCAGCAGCAGGGTGGGAGAGAAGCTCCAGTCAGCCCACAA
GATGCCATTGTCCCCCGGCCTCCTGCTGCTGCTGCTCTCCGGGGCCACGGCCACCGCTGCCCT
GCCCCTGGAGGGTGGCCCCACCGGCCGAGACAGCGAGCATATGCAGGAAGCGGCAGGAATAAG
GAAAAGCAGCCTCCTGACTTTCCTCGCTTGGTGGTTTGAGTGGACCTCCCAGGCCAGTGCCGG
GCCCCTCATAGGAGAGGAAGCTCGGGAGGTGGCCAGGCGGCAGGAAGGCGCACCCCCCAGCA
ATCCGCGCGCCGGGACAGAATGCCCTGCAGGAACCTTCTTCTGGAAGACCTTCTCCTCCTGCAA
ATAG

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FIGURE 380

MYRHKNSWRLGLKYPPSSKEETQVPKTLISGLPGRKSSSRVGEKLQSAHKMPLSPGLLLLLLS
GATATAALPLEGGPTGRDSEHMQEAAGIRKSSLLTFLAWWFEWTSQASAGPLIGEEAREVARR
QEGAPPQQSARRDRMPCRNFFWKTFSSCK

Important features:**Transmembrane domain:**

amino acids 51-69

cAMP- and cGMP-dependent protein kinase phosphorylation sites.

amino acids 35-39, 92-96

N-myristoylation sites.

amino acids 64-70, 75-81, 90-96

Amidation site.

amino acids 33-37

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FIGURE 381

GGCGCCGGTGCACCGGGCGGGCTGAGCGCCTCCTGCGGCCCGGCCTGCGCGCCCCGGCCCGCC
GCGCCGCCCCACGCCCCAACCCCGGCCCGCGCCCCCTAGCCCCCGCCCCGGGCCCGCGCCCCGCGC
CCGCGCCCAGGTGAGCGCTCCGCCCGCCGCGAGGCCCGCCCCGGCCCCGCCCCGCCCCGCCCC
CGGCCGGCGGGGGAACCGGGCGGATTCTCGCGCGTCAAACACCTGATCCCATAAAACATTC
ATCCTCCCGGCGGCCCGCGCTGCGAGCGCCCCGCCAGTCCGCGCCGCGCCGCCCTCGCCCTG
TGCGCCCTGCGCGCCCTGCGCACCCGCGGCCCGAGCCCAGCCAGAGCCGGGCGGAGCGGAGCG
CGCCGAGCCTCGTCCCGCGGCCGGGCCGGGGCCGGGCCGTAGCGGCGGGCGCCTGGATGCGGAC
CCGGCCGCGGGGAGACGGGCGCCCCGCCCCGAAACGACTTTCAGTCCCCGACGCGCCCCGCCCA
ACCCCTACG**ATGA**AGAGGGCGTCCGCTGGAGGGAGCCGGCTGCTGGCATGGGTGCTGTGGCTG
CAGGCCTGGCAGGTGGCAGCCCCATGCCCAGGTGCCTGCGTATGCTACAATGAGCCCAAGGTG
ACGACAAGCTGCCCCCAGCAGGGCCTGCAGGCTGTGCCCGTGGGCATCCCTGCTGCCAGCCAG
CGCATCTTCTTGACAGGCAACCGCATCTCGCATGTGCCAGCTGCCAGCTTCCGTGCCTGCCGC
AACCTCACCATCCTGTGGCTGCACTCGAATGTGCTGGCCCCGAATTGATGCGGCTGCCTTCACT
GGCCTGGCCCTCCTGGAGCAGCTGGACCTCAGCGATAATGCACAGCTCCGGTCTGTGGACCCT
GCCACATTCCACGGCCTGGGCCGCGCTACACACGCTGCACCTGGACCGCTGCGGCCTGCAGGAG
CTGGGCCCCGGGGCTGTTCCGCGGCCTGGCTGCCCTGCAGTACCTCTACCTGCAGGACAACGCG
CTGCAGGCACTGCCTGATGACACCTTCCGCGACCTGGGCAACCTCACACACCTCTTCTGAC
GGCAACCGCATCTCCAGCGTGCCCGAGCGCGCCTTCCGTGGGCTGCACAGCCTCGACCGTCTC
CTACTGCACCAGAACC CGTGCGGCCATGTGCACCCGCATGCCTTCCGTGACCTTGGCCGCTC
ATGACACTCTATCTGTTTGCCAACAATCTATCAGCGCTGCCCCTGAGGCCCTGGCCCCCTG
CGTGCCCTGCAGTACCTGAGGCTCAACGACAACCCCTGGGTGTGTGACTGCCGGGCACGCCCA
CTCTGGGCCTGGCTGCAGAAGTTCCGCGGCTCCTCCTCCGAGGTGCCCTGCAGCCTCCCGCAA
CGCCTGGCTGGCCGTGACCTCAAACGCCTAGCTGCCAATGACCTGCAGGGCTGCGCTGTGGCC
ACCGGCCCTTACCATCCCATCTGGACCGGCAGGGCCACCGATGAGGAGCCGCTGGGGCTTCCC
AAGTGCTGCCAGCCAGATGCCGCTGACAAGGCCTCAGTACTGGAGCCTGGAAGACCAGCTTCG
GCAGGCAATGCGCTGAAGGGACGCGTGCCGCCCGGTGACAGCCCGCCGGGCAACGGCTCTGGC
CCACGGCACATCAATGACTCACCCTTTGGGACTCTGCCTGGCTCTGCTGAGCCCCCGCTCACT
GCAGTGCGGCCCGAGGGCTCCGAGCCACCAGGGTTCCCCACCTCGGGCCCTCGCCGGAGGCCA
GGCTGTTACGCAAGAACC GCACCCGCAGCCACTGCCGTCTGGGCCAGGCAGGCAGCGGGGT
GGCGGGACTGGTGACTCAGAAGGCTCAGGTGCCCTACCCAGCCTCACCTGCAGCCTCACCCCC
CTGGGCCTGGCGCTGGTGCTGTGGACAGTGCTTGGGCCCTGCT**TGA**CCCCCAGCGGACACAAGA
GCGTGCTCAGCAGCCAGGTGTGTGTACATACGGGGTCTCTCTCCACGCCGCCAAGCCAGCCGG
GCGGCCGACCCGTGGGGCAGGCCAGGCCAGGTCTCTCCCTGATGGACGCCTGCCGCCCGCCACC
CCCATCTCCACCCCATCATGTTTACAGGGTTCGGCGGCAGCGTTTGTTCAGAACGCCGCTC
CCACCCAGATCGCGGTATATAGAGATATGCATTTTATTTTACTTGTGTAAAAATATCGGACGA
CGTGGAATAAAGAGCTCTTTTCTTAAAAAA

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FIGURE 382

MKRASAGGSRL LAWVLWLQAWQVAAPCPGACVCYNEPKVTTSCPQQGLQAVPVGIPAASQRI F
LHG NRISHVPAASFRACRNLTILWLHSNVLARIDAAAF TGLALLEQLDLSDNAQLRSVDPATF
HGLGRLHTLHLDRCG LQELGPGLFRGLAALQYLYLQDNALQALPDDTFRDLGNLTHLFLHG NR
ISSVPERAFRGLHSLDRLLLHQNRVAHVH PHAFRDLGRLMTLYLFANNLSALPTEALAPLRAL
QYLR LNDNPWVCD CRARPLWAWLQKFRGSSSEVPCSLPQRLAGRDLKRLAANDLQGCAVATGP
YHPIWTGRATDEEPLGLPKCCQPDAA DKASVLEPGRPASAGNALKGRVPPGDSPPGNGSGPRH
INDSPFGTLPGSAEPPLTAVRPEGSEPPGFPTSGPRRRPGCSRKNRTRSHCRLGQAGSGGGGT
GDSEGS GALPSLTCSLTPLGLALVLWTVLGPC

Important features:**Signal peptide:**

amino acids 1-26

Leucine zipper pattern.

amino acids 135-156

Glycosaminoglycan attachment site.

amino acids 436-439

N-glycosylation site.

amino acids 82-85, 179-183, 237-240, 372-375 and 423-426

VWFC domain

amino acids 411-425

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FIGURE 383

TTCGTGACCCTTGAGAAAAGAGTTGGTGGTAAATGTGCCACGTCTTCTAAGAAGGGGGAGTCTGAACTTGTCTG
AAGCCCTTGTCGTAAGCCTTGAACCTACGTTCTTAAATCTATGAAGTCGAGGGACCTTTGCTGCTTTTGTAGGG
ACTTCTTTCCTTGCTTCAGCAAC**ATG**AGGCTTTTCTTGTGGAACGCGGTCTTGACTCTGTTGCTCACTTCTTTGA
TTGGGGCTTTGATCCCTGAACCAGAAGTGAAAATTGAAGTTCTCCAGAAGCCATTCATCTGCCATCGCAAGACCA
AAGGAGGGGATTTGATGTTGGTCCACTATGAAGGCTACTTAGAAAAGGACGGCTCCTTATTTCACTCCACTCACA
AACATAACAATGGTCAGCCCATTTGGTTTACCCTGGGCATCCTGGAGGCTCTCAAAGGTTGGGACCAGGGCTTGA
AAGGAATGTGTGTAGGAGAGAAGAGAAAGCTCATCATTCCTCCTGCTCTGGGCTATGGAAAAGAAGGAAAAGGTA
AAATTCCCCCAGAAAAGTACACTGATATTTAATATTGATCTCCTGGAGATTGAAATGGACCAAGATCCCATGAAT
CATTCCAAGAAATGGATCTTAATGATGACTGGAACTCTCTAAAGATGAGGTTAAAGCATATTTAAAGAAGGAGT
TTGAAAACATGGTGCGGTGGTGAATGAAAGTCATCATGATGCTTTGGTGGAGGATATTTTTGATAAAGAAGATG
AAGACAAAGATGGGTTTATATCTGCCAGAGAATTTACATATAAACACGATGAGTTA**TAG**AGATACATCTACCCTT
TTAATATAGCACTCATCTTTCAAGAGAGGGCAGTCATCTTTAAAGAACATTTTATTTTTATACAATGTTCTTTCT
TGCTTTGTTTTTATTTTTATATATTTTTCTGACTCCTATTTAAAGAACCCCTTAGGTTTCTAAGTACCCATTT
CTTTCTGATAAGTTATTGGGAAGAAAAGCTAATTGGTCTTTGAATAGAAGACTTCTGGACAATTTTTCACTTTC
ACAGATATGAAGCTTTGTTTTACTTTCTCACTTATAAATTTAAATGTTGCAACTGGGAATATACCACGACATGA
GACCAGGTTATAGCACAAATTAGCACCTTATATTTCTGCTTCCCTCTATTTTCTCCAAGTTAGAGGTCAACATTT
GAAAAGCCTTTTGCAATAGCCCAAGGCTTGCTATTTTCATGTTATAATGAAATAGTTTATGTGTAAGTGGCTCTG
AGTCTCTGCTTGAGGACCAGAGGAAAATGGTTGTTGGACCTGACTTGTTAATGGCTACTGCTTTACTAAGGAGAT
GTGCAATGCTGAAGTTAGAAACAAGGTTAATAGCCAGGCATGGTGGCTCATGCCTGTAATCCCAGCACTTTGGGA
GGCTGAGGCGGGCGGATCACCTGAGGTTGGGAGTTCGAGACCAGCCTGACCAACACGGAGAAACCCTATCTCTAC
TAAAAATACAAAGTAGCCCGGCGTGGTGATGCGTGCCTGTAATCCCAGCTACCCAGGAAGGCTGAGGCGGCAGAA
TCACTTGAACCCGAGGCCGAGGTTGCGGTAAGCCGAGATCACCTNCAGCCTGGACACTCTGTCTCGAAAAAAGAA
AAGAACACGGTTAATACCATATNAATATGTATGCATTGAGACATGCTACCTAGGACTTAAGCTGATGAAGCTTGG
CTCCTAGTGATTGGTGGCCTATTATGATAAATAGGACAAATCATTTATGTGTGAGTTTCTTTGTAATAAAATGTA
TCAATATGTTATAGATGAGGTAGAAAGTTATATTTATATTCAATATTTACTTCTTAAGGCTAGCGGAATATCCTT
CCTGGTTCTTTAATGGGTAGTCTATAGTATATTATACTACAATAACATTGTATCATAAGATAAAGTAGTAAACCA
GTCTACATTTTCCCATTTCTGTCTCATCAAAAAGTGAAGTTAGCTGGGTGTGGTGGCTCATGCCTGTAATCCCAG
CACTTTGGGGGCCAAGGAGGGTGGATCACTTGAGATCAGGAGTTCAAGACCAGCCTGGCCAACATGGTGAAACCT
TGTCTCTACTAAAAATACAAAAATTAGCCAGGCGTGGTGGTGCACACCTGTAGTCCCAGCTACTCGGGAGGCTGA
GACAGGAGATTTGCTTGAACCCGGGAGGCGGAGGTTGCAGTGAGCCAAGATTGTGCCACTGCACTCCAGCCTGGG
TGACAGAGCAAGACTCCATCTCAAAAAAAAAAAAAAGAAGCAGACCTACAGCAGCTACTATTGAATAAATACCTA
TCCTGGATTTT

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FIGURE 384

MRLFLWNAVLTLFVTSLLIGALIPPEVKIEVLQKPFICHRKTKGGDLMLVHYEGYLEKDGS LF
HSTHKHNNGQPIWFTLGILEALKGWDQGLKGMCVGEKRKLIIPPALGYGKEGKGKIPPESTLI
FNIDLLEIRNGPRSHESFQEMDLNDDWKLSKDEVKAYLKKEFEKKGAVVNESHHDALVEDIFD
KEDEDKDGFI SAREFTYKHDEL

Important features:**Signal peptide:**

amino acids 1-20

N-glycosylation site.

amino acids 176-179

Casein kinase II phosphorylation site.

amino acids 143-146, 156-159, 178-181 and 200-203

Endoplasmic reticulum targeting sequence.

amino acids 208-211

FKBP-type peptidyl-prolyl cis-trans isomerase

amino acids 78-114 and 118-131

EF-hand calcium-binding domain.

amino acids 191-203, 184-203 and 140-159

S-100/ICaBP type calcium binding domain

amino acids 183-203

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FIGURE 385

CTCCACGGTGTCCAGCGCCCAGAA**ATG**CGGCTTCTGGTCCTGCTATGGGGTTGCCTGCTGCTC
CCAGGTTATGAAGCCCTGGAGGGCCCAGAGGAAATCAGCGGGTTCGAAGGGGACACTGTGTCC
CTGCAGTGCACCTACAGGGAAGAGCTGAGGGACCACCGGAAGTACTGGTGCAGGAAGGGTGGG
ATCCTCTTCTCTCGCTGCTCTGGCACCATCTATGCAGAAGAAGAAGGCCAGGAGACAATGAAG
GGCAGGGTGTCCATCCGTGACAGCCGCCAGGAGCTCTCGCTCATTGTGACCCTGTGGAACCTC
ACCCTGCAAGACGCTGGGGAGTACTGGTGTGGGGTCGAAAAACGGGGCCCCGATGAGTCTTTA
CTGATCTCTCTGTTCTGTTTCCAGGACCCTGCTGTCCTCCCTCCCCTTCTCCACCTTCCAG
CCTCTGGCTACAACACGCCTGCAGCCCCAAGGCAAAAGCTCAGCAAACCCAGCCCCCAGGATTG
ACTTCTCCTGGGCTCTACCCGGCAGCCACCACAGCCAAGCAGGGGAAGACAGGGGCTGAGGCC
CCTCCATTGCCAGGGACTTCCCAGTACGGGCACGAAAGGACTTCTCAGTACACAGGAACCTCT
CCTCACCCAGCGACCTCTCCTCCTGCAGGGAGCTCCCGCCCCCCCCATGCAGCTGGACTCCACC
TCAGCAGAGGACACCAGTCCAGCTCTCAGCAGTGGCAGCTCTAAGCCCAGGGTGTCCATCCCG
ATGGTCCGCATACTGGCCCCAGTCCTGGTGTGCTGAGCCTTCTGTTCAGCCGCAGGCCTGATC
GCCTTCTGCAGCCACCTGCTCCTGTGGAGAAAGGAAGCTCAACAGGCCACGGAGACACAGAGG
AACGAGAAGTTCTGGCTCTCACGCTTGACTGCGGAGGAAAAGGAAGCCCCCTTCCCAGGCCCT
GAGGGGGACGTGATCTCGATGCCTCCCCCTCCACACATCTGAGGAGGAGCTGGGCTTCTCGAAG
TTTGTCTCAGCG**TAG**GGGCAGGAGGCCCTCCTGGCCAGGCCAGCAGTGAAGCAGTATGGCTGGC
TGGATCAGCACCGATTCCCGAAAGCTTTCCACCTCAGCCTCAGAGTCCAGCTGCCCGGACTCC
AGGGCTCTCCCCACCCTCCCCAGGCTCTCCTCTTGCATGTTCCAGCCTGACCTAGAAGCGTTT
GTCAGCCCTGGAGCCCAGAGCGGTGGCCTTGCTCTTCCGGCTGGAGACTGGGACATCCCTGAT
AGGTTACATCCCTGGGCAGAGTACCAGGCTGCTGACCCTCAGCAGGGCCAGACAAGGCTCAG
TGGATCTGGTCTGAGTTTCAATCTGCCAGGAACTCCTGGGCCTCATGCCCAGTGTGCGACCCCT
GCCTTCTCCCACTCCAGACCCACCTTGTCTTCCCTCCCTGGCGTCTCAGACTTAGTCCCA
CGGTCTCCTGCATCAGCTGGTGTGATGAAGAGGAGCATGCTGGGGTGAGACTGGGATTCTGGCTT
CTCTTTGAACCACCTGCATCCAGCCCTTCAGGAAGCCTGTGAAAAACGTGATTCTGGCCCCA
CCAAGACCCACCAAAACCATCTCTGGGCTTGGTGCAGGACTCTGAATTCTAACAATGCCCAGT
GACTGTGCACTTGAGTTTGAGGGCCAGTGGGCCTGATGAACGCTCACACCCCTTCAGCTTAG
AGTCTGCATTTGGGCTGTGACGTCTCCACCTGCCCAATAGATCTGCTCTGTCTGCGACACCA
GATCCACGTGGGGACTCCCCTGAGGCCTGCTAAGTCCAGGCCTTGGTCAGGTCAGGTGCACAT
TGCAGGATAAGCCCAGGACCGGCACAGAAGTGGTTGCCTTTNCCATTTGCCCTCCCTGGNCCA
TGCCTTCTTGCCTTTGGAAAAAATGATGAAGAAAACCTTGGCTCCTTCCCTTGTCTGGAAAGGG
TTACTTGCCTATGGGTTCTGGTGGCTAGAGAGAAAAGTAGAAAACCAGAGTGCACGTAGGTGT
CTAACACAGAGGAGAGTAGGAACAGGGCGGATACCTGAAGGTGACTCCGAGTCCAGCCCCCTG
GAGAAGGGGTGCGGGGTGGTGGTAAAGTAGCACAACTACTATTTTTTTTCTTTTTTCCATTATT
ATTGTTTTTTAAGACAGAATCTCGTGCTGCTGCCCAGGCTGGAGTGCAGTGGCACGATCTGCA
AACTCCGCCTCCTGGGTTCAAGTGATTCTTCTGCCTCAGCCTCCCGAGTAGCTGGGATTACAG
GCACGCACCACCACACCTGGCTAATTTTTGTACTTTTAGTAGAGATGGGGTTTTACCATGTTG
GCCAGGCTGGTCTTGAACCTCCTGACCTCAAATGAGCCTCCTGCTTCAGTCTCCCAAATTGCCG
GGATTACAGGCATGAGCCACTGTGTCTGGCCCTATTTCTTTAAAAAGTGAAATTAAGAGTTG
TTCAGTATGCAAACTTGGAAAGATGGAGGAGAAAAAGAAAGGAAGAAAAAATGTCACCCA
TAGTCTCACCAGAGACTATCATTATTTGTTTTGTTGTACTTCCTTCCACTCTTTTCTTCTTC
ACATAATTTGCCGGTGTTCTTTTTTACAGAGCAATTATCTTGTATATACAACCTTTGTATCCTGC
CTTTTCCACCTTATCGTTCCATCACTTTATTCCAGCACTTCTCTGTGTTTTTACAGACCTTTTT
ATAAATAAAATGTTTCATCAGCTGCATAAAAAAAAAAAAAA

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FIGURE 386

MRLLVLLWGCLLLPGYEALEGPTEEISGFEGDTVSLQCTYREELRDHRKYWCRKGGILFSRCSG
TIYAEEEGQETMKGRVSIIRDSRQELSLIVTLWNLTLDAGEYWCGVEKRGPDSELLISLFVFP
GPCCPPSPSPTFQPLATTRLQPKAKAQQQTQPPGLTSPGLYPAATTAKQGKTGAEAPPLPGTSQ
YGHERTSQYTGTSPHPATSPPAGSSRPPMQLDSTSAEDTSPALSSGSSKPRVSI PMVRILAPV
LVLLSLLSAAGLIAFCSHLLLWRKEAQQATETQRNEKFWLSRLTAEKEAPSQAPEGDVISM
PLHTSEEELGFSKFVSA

Important features:**Signal peptide:**

amino acids 1-17

Transmembrane domain:

amino acids 248-269

N-glycosylation site.

amino acids 96-99

Fibrinogen beta and gamma chains C-terminal domain.

amino acids 104-113

Ig like V-type domain:

amino acids 13-128

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FIGURE 387

GCGCCGGGAGCCCATCTGCCCCCAGGGGCACGGGGCGCGGGGCGGGCTCCCGCCCGGCACATG
GCTGCAGCCACCTCGCGCGCACCCCGAGGGCGCCGCGCCCGAGCTCGCCCGAGGTCCGTTCGGAGG
CGCCCGGCCGCCCCGGAGCCAAGCAGCAACTGAGCGGGGAAGCGCCCGCGTCCGGGGATCGGG
ATGTCCCTCCTCCTTCTCCTCCTTGCTAGTTTCTACTATGTTGGAACCTTGGGGACTCACACT
GAGATCAAGAGAGTGGCAGAGGAAAAGGTCACCTTGGCCCTGCCACCATCAACTGGGGCTTCCA
GAAAAAGACACTCTGGATATTGAATGGCTGCTCACCGATAATGAAGGGAACCAAAGTGGTG
ATCACTTACTCCAGTCGTCATGTCTACAATAACTTGACTGAGGAACAGAAGGGCCGAGTGGCC
TTTGCTTCCAATTTCTGGCAGGAGATGCCTCCTTGACAGATTGAACCTCTGAAGCCAGTGAT
GAGGGCCGGTACACCTGTAAGGTTAAGAATTCAGGGCGCTACGTGTGGAGCCATGTCATCTTA
AAAGTCTTAGTGAGACCATCCAAGCCCAAGTGTGAGTTGGAAGGAGAGCTGACAGAAGGAAGT
GACCTGACTTTGCAGTGTGAGTCATCCTCTGGCACAGAGCCCATTGTGTATTACTGGCAGCGA
ATCCGAGAGAAAAGAGGGAGAGGATGAACGTCTGCCTCCCAAATCTAGGATTGACTACAACCAC
CCTGGACGAGTTCTGCTGCAGAACTTACCATGTCCTACTCTGGACTGTACCAGTGCACAGCA
GGCAACGAAGCTGGGAAGGAAAGCTGTGTGGTGGCAGTAACCTGTACAGTATGTACAAAGCATC
GGCATGGTTGCAGGAGCAGTGACAGGCATAGTGGCTGGAGCCCTGCTGATTTTCTCCTTGGTG
TGGCTGCTAATCCGAAGGAAAGACAAAGAAAGATATGAGGAAGAAGAGAGACCTAATGAAATT
CGAGAAGATGCTGAAGCTCCAAAAGCCCGTCTTGTGAAACCCAGCTCCTCCTCCTCAGGCTCT
CGGAGCTCACGCTCTGGTTCTTCTCCACTCGCTCCACAGCAAATAGTGCCTCACGCAGCCAG
CGGACACTGTCAACTGACGCAGCACCCAGCCAGGGCTGGCCACCCAGGCATACAGCCTAGTG
GGGCCAGAGGTGAGAGGTTCTGAACCAAAGAAAGTCCACCATGCTAATCTGACCAAAGCAGAA
ACCACACCCAGCATGATCCCCAGCCAGAGCAGAGCCTTCCAAACGGTCT**TGA**ATTACAATGGAC
TTGACTCCCACGCTTTCCTAGGAGTCAGGGTCTTTGGACTCTTCTCGTCATTGGAGCTCAAGT
CACCAGCCACACAACCAGATGAGAGGTCATCTAAGTAGCAGTGAGCATTGCACGGAACAGATT
CAGATGAGCATTTTCTTATACAATAACCAAACAAGCAAAAGGATGTAAGCTGATTTCATCTGTA
AAAAGGCATCTTATTGTGCCTTTAGACCAGAGTAAGGGAAAGCAGGAGTCCAAATCTATTTGT
TGACCAGGACCTGTGGTGAGAAGGTTGGGGAAAGGTGAGGTGAATATACCTAAAACCTTTTAAT
GTGGGATATTTTGTATCAGTGCTTTGATTCACAATTTTCAAGAGGAAATGGGATGCTGTTTGT
AAATTTTCTATGCATTTCTGCAAACTTATTGGATTATTAGTTATTCAGACAGTCAAGCAGAAC
CCACAGCCTTATTACACCTGTCTACACCATGTACTGAGCTAACCCTTCTAAGAACTCCAAA
AAAGGAAACATGTGTCTTCTATTCTGACTTAACCTTCATTTGTCATAAGGTTTGGATATTAATT
TCAAGGGGAGTTGAAATAGTGGGAGATGGAGAAGAGTGAATGAGTTTCTCCCACTCTATACTA
ATCTCACTATTTGTATTGAGCCCAAAATAACTATGAAAGGAGACAAAAATTTGTGACAAAGGA
TTGTGAAGAGCTTTCCATCTTCATGATGTTATGAGGATTGTTGACAAACATTAGAAATATATA
ATGGAGCAATTGTGGATTTCCCTCAAATCAGATGCCTCTAAGGACTTTCCTGCTAGATATTT
CTGGAAGGAGAAAATACAACATGTCAATTTATCAACGTCCTTAGAAAGAATTCTTCTAGAGAAA
AAGGGATCTAGGAATGCTGAAAGATTACCCAACATACCATTATAGTCTCTTCTTCTGAGAAA
ATGTGAAACCAGAATTGCAAGACTGGGTGGACTAGAAAGGGAGATTAGATCAGTTTTCTCTTA
ATATGTCAAGGAAGGTAGCCGGGCATGGTGCCAGGCACCTGTAGGAAAATCCAGCAGGTGGAG
GTTGCAGTGAGCCGAGATTATGCCATTGCACTCCAGCCTGGGTGACAGAGCGGGACTCCGTCTC

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FIGURE 388

MSLLLLLLLLVSYYVGTLGTHTEIKRVAEEKVTLPCHHQLGLPEKDTLDIEWLLTDNEGNQKVV
ITYSSRHVYNNLTEEQKGRVAFASNFLAGDASLQIEPLKPSDEGRYTCKVKNSGRYVWSHVIL
KVLVRPSKPKCELEGELTEGSDLTLCESSTGTEPIVYYWQRIREKEGEDERLPPKSRIDYNH
PGRVLLQNLTMSSGLYQCTAGNEAGKESCVVRVTVQYVQSIGMVAGAVTGIVAGALLIFLLV
WLLIRRKDKERYEEEEERPNEIREDAEAPKARLVKPSSSSSSGSRSSRSGSSSTRSTANSASRSQ
RTLSTDAAPQPGLATQAYSLVGPEVRGSEPKKVHHANLTKAETTPSMIPSQSRAFQTV

Important features:**Signal sequence:**

amino acids 1-16

Transmembrane domain:

amino acids 232-251

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FIGURE 389

GCGGCACCTGGAAG**ATG**CGCCCATTTGGCTGGTGGCCTGCTCAAGGTGGTGTTCGTGGTCTTCG
CCTCCTTGTGTGCCTGGTATTTCGGGGTACCTGCTCGCAGAGCTCATTCCAGATGCACCCCTGT
CCAGTGCTGCCTATAGCATCCGCAGCATCGGGGAGAGGCCTGTCCTCAAAGCTCCAGTCCCCA
AAAGGCAAAAATGTGACCACTGGACTCCCTGCCCATCTGACACCTATGCCTACAGGTACTCA
GCGGAGGTGGCAGAAGCAAGTACGCCAAAATCTGCTTTGAGGATAACCTACTTATGGGAGAAC
AGCTGGGAAATGTTGCCAGAGGAATAAACATTGCCATTGTCAACTATGTAAGTGGGAATGTGA
CAGCAACACGATGTTTTGATATGTATGAAGGCGATAACTCTGGACCGATGACAAAGTTTATTC
AGAGTGCTGCTCCAAAATCCCTGCTCTTCATGGTGACCTATGACGACGGAAGCACAAGACTGA
ATAACGATGCCAAGAATGCCATAGAAGCACTTGGAAGTAAAGAAATCAGGAACATGAAATTCA
GGTCTAGCTGGGTATTTATTGCAGCAAAAGGCTTGGAAGTCCCTTCCGAAATTCAGAGAGAAA
AGATCAACCACTCTGATGCTAAGAACAACAGATATTCTGGCTGGCCTGCAGAGATCCAGATAG
AAGGCTGCATACCCAAAGAACGAAGC**TGA**CACTGCAGGGTCCTGAGTAAATGTGTTCTGTATA
AACAAATGCAGCTGGAATCGCTCAAGAATCTTATTTTTCTAAATCCAACAGCCCATATTTGAT
GAGTATTTTGGGTTTGTGTAAACCAATGAACATTTGCTAGTTGTATCAAATCTTGGTACGCA
GTATTTTTTATACCAGTATTTTATGTAGTGAAGATGTCAATTAGCAGGAACTAAAATGAATGG
AAATTCTTAAAAAAAAA

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FIGURE 390

MRPLAGGLLKVVVFVVFASLCAWYSGYLLAELIPDAPLSSAAYSIRSIGERPVLKAPVPKRQKC
DHWTPCPSDTYAYRLLSGGGRSKYAKICFEDNLLMGEQLGNVARGINIAIVNYVTGNVTATRC
FDMYEGDNSGPMTKFIQSAAPKSLLFMVTYDDGSTRLNNDKNAIEALGSKEIRNMKFRSSWV
FIAAKGLELPSEIQREKINHSDAKNNRYSGWPAEIQIEGCIPKERS

Important features:**Signal sequence.**

amino acids 1-20

N-glycosylation sites.

amino acids 120-124, 208-212

Glycosaminoglycan attachment site.

amino acids 80-84

N-myristoylation sites.

amino acids 81-87, 108-114, 119-125

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FIGURE 391

GGGGGCTTTCTTGGGCTTGGCTGCTTGGAAACCTGCTTCCAAGGACCGGCCTCGGAGGGGTCGCCGGGAAAGGG
AGGGAAGAAGGAAGGGCGGGCCGGCCCCCTGCGCCCGCCCGCGCCTCTGCGCGCCCCCTGTCCGCCCCGGCCC
AGCCCCAGCCCAGCCCCGCGGGCCGGTACACGCGCAGCCAGCCGGCCGCTCCCGCGCCCAAGCGCGCCGCTCTG
CTGTGCCCTGCGCCCTTGCCCCGCGCCAGCTTCTGCGCCCGCAGCCCGCCCGGCGCCCCCGGTGACCGTGACCCT
GCCCTGGGCGCGGGGCGGAGCAGGC**ATGT**CCCCCGCGGGGACCCTACCCAGCGCTGGCCCTGGTGCTCCTGGC
AGTGACCCTGGCCGGGGTCGGAGCCCAGGGCGCAGCCCTCGAGGACCCTGATTATTACGGGCAGGAGATCTGGAG
CCGGGAGCCCTACTACGCGCGCCCGGAGCCCGAGCTCGAGACCTTCTCTCCGCGCTGCCTGCGGGGCCCCGGGA
GGAGTGGGAGCGGCGCCCGCAGGAGCCCAGGCCGCCAAGAGGGCCACCAAGCCCAAGAAAGCTCCCAAGAGGGA
GAAGTCGGCTCCCGAGCCGCTCCACCAGGTAAACACAGCAACAAAAAAGTTATGAGAACCAAGAGCTCTGAGAA
GGCTGCCAACGATGATCACAGTGTCCGTGTGGCCCGTGAAGATGTGAGAGAGAGTTGCCACCTCTTGGTCTGGA
AACCTTAAAAATCACAGACTTCCAGCTCCATGCCTCCACGGTGAAGCGCTATGGCCTGGGGGCACATCGAGGGAG
ACTCAACATCCAGGCGGGCATTAAATGAAAATGATTTTATGACGGAGCGTGGTGCGCGGGAAGAAATGACCTCCA
GCAGTGGATTGAAGTGGATGCTCGGCGCCTGACCAGATTCACTGGTGTCACTCAAGGGAGGAACTCCCTCTG
GCTGAGTGACTGGGTGACATCCTATAAGGTGATGGTGAGCAATGACAGCCACACGTGGGTCACTGTTAAGAATGG
ATCTGGAGACATGATATTTGAGGGAAACAGTGAGAAAGGAGATCCCTGTTCTCAATGAGCTACCCGTCCCCATGGT
GGCCCCGTACATCCGCATAAACCCCTCAGTCCTGGTTTGATAATGGGAGCATCTGCATGAGAATGGAGATCCTGGG
CTGCCCCACTGCCAGATCCTAATAATTATTATCACCGCCGGAACGAGATGACCACCACTGATGACCTGGATTTTAA
GCACCACAATTATAAGGAAATGCGCCAGTTGATGAAAGTTGTGAATGAAATGTGTCCCAATATCACCCAGAATTTA
CAACATTGGAAAAAGCCACCAGGGCCTGAAGCTGTATGCTGTGGAGATCTCAGATCACCTGGGGAGCATGAAGT
CGGTGAGCCCGAGTTCCACTACATCGCGGGGGCCACGGCAATGAGGTGCTGGGCCGGGAGCTGCTGCTGCTGCT
GGTGCACTTCGTGTGTGAGGAGTACTTGGCCCGGAATGCGCGCATCGTCCACCTGGTGGAGGAGACGCGGATTCA
CGTCTCCCCCTCCCTCAACCCCGATGGCTACGAGAAGGCCTACGAAGGGGGCTCGGAGCTGGGAGGCTGGTCCCT
GGGACGCTGGACCCACGATGGAATTGACATCAACAACAACCTTCTGATTTAAACACGCTGCTCTGGGAGGCAGA
GGATCGACAGAATGTCCCCAGGAAAGTTCCCAATCACTATATTGCAATCCCTGAGTGGTTTTCTGTGCGAAAATGC
CACGGTGGCTGCCGAGACCAGAGCAGTCATAGCCTGGATGGAAAAAATCCCTTTTGTGCTGGGCGGCAACCTGCA
GGGCGGCGAGCTGGTGGTGGCGTATCCCTACGACCTGGTGCGGTCCCCCTGGAAGACGACAGAACACACCCCCAA
CCCCGATGACCACGTGTTCCGCTGGCTGGCCTACTCCTATGCCTCCACACACCCGCTCATGACAGACGCCCGGAG
GAGGGTGTGCCACACGGAGGACTTCCAGAAGGAGGAGGGCACTGTCAATGGGGCCTCCTGGCACACCGTCGCTGG
AAGTCTGAACGATTTGAGCTACCTTCATACAAACTGCTTCGAACTGTCCATCTACGTGGGCTGTGATAAATACCC
ACATGAGAGCCAGCTGCCCCAGGAGTGGGAGAATAACCGGGAATCTCTGATCGTGTTCATGGAGCAGGTTTCATCG
TGGCATTAAAGGCTTGGTGAGAGATTACATGGAAAAAGGAATCCCAAACGCCATTATCTCCGTAGAAGGCATTAA
CCATGACATCCGAACAGCCAACGATGGGGATTACTGGCGCCTCCTGAACCCTGGAGAGTATGGTGCACAGCAAA
GGCCGAAGGTTTCACTGCATCCACCAAGAAGTGTATGGTTGGCTATGACATGGGGGCCAAGGTGTGACTTTCAC
ACTTAGCAAAACCAACATGGCCAGGATCCGAGAGATCATGGAGAAGTTTGGGAAGCAGCCCGTCAGCCTGCCAGC
CAGGCGGCTGAAGCTGCGGGGGCGGAAGAGACGACAGCGTGGG**TGAC**CCCTCCTGGGCCCTTGAGACTCGTCTGGG
ACCCATGCAAATTAACCAACCTGGTAGTAGCTCCATAGTGGAAGTCACTCACTGTTGTTTCTCTGTAATTCAG
AAGTGCCTGGAAGAGAGGGTGCATTGTGAGGCAGGTCCCAAAAGGGAAGGCTGGAGGCTGAGGCTGTTTTCTTTT
CTTTGTTCCCATTTATCCAAATAACTTGGACAGAGCAGCAGAGAAAAGCTGATGGGAGTGAGAGAACTCAGCAAG
CCAACCTGGGAATCAGAGAGAGAAGGAGAAGGAGGGGAGCCTGTCCGTTGAGAGCCTCTGGCTGCATAGAAAAGG
ATTCTGGTGCTTCCCCTGTTTGGCTGGCAGCAAGGGTCCACGTGCATTTGCAATTTGCACAGCTAAAATTGCAG
CATTTCCCCAGCTGGGCTGTCCCAATGTTACCATTTGAGATGCTCCAGGCGTCCTAAGAGAATCCACCCTCTC
TGGCCCTGGGACATTGCAAGCTGCTACAAATAAATTCTGTGTCTTTTGACAATAGCGTCATTGCCAAGTGCACA
TCAGTGAGCCTCTTGAATCTGTTTAGTCTCCTTTTTCAACAAAGGAGTGTGTTGAGAAAAGGAGAGAGAGGCTGA
GATCATTACGAGTGTGTTGGGCAGCAAGCATGGAGCTTCTGCACAAATCTGGGTCCATAAACAACCCCCAAA
GTCCCTGCTGATCCAGTAGCCCTGGAGGTTCCCCAGGTAGGGAGAGCCAGAGGTGCCAGCCTTCTGAAGGGCCA
GAAAATTTAGCCTGGATCTCCTCTTTTACCTGCTAGGACTGGAAAGAGCCAGAAGTGGGGTGGCCTGAAGCCCTC
TCTCTGCTTGAGGTATTGCCCTGTGTGGAATTGAGTGCTCATGGGTGGCCTCATATCAGCCTGGGAGTTATTT
TTGATATGTAGAATGCCAGATCTCCAGATTAGGCTAAATGTAATGAAAACCTCTTAGGATTATCTGTGGAGCAT
CAGTTTGGGAAGAATTATTGAATTATCTTGCAAGAAAAAGTATGTCTCACTTTTTGTTAATGTTGCTGCCTCAT
TGACCTGGGAAAAATGAAAAAAAATAAAGCAAATGGTAAGACCCTTAAAAAAAATGTTGCTGCCTCAT
AAAAAAAAAAAAAAAAAAAAA

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FIGURE 392

MSRPGTATPALALVLLAYTLAGVGAQGAALEDPDYYGQEIWSREPYYARPEPELETFSPPLPA
GPGEEWERRPQEPRPPKRATKPKKAPKREKSAPEPPPPGKHSNKKVMRTKSSEKAANDDHVR
VAREDVRESCPPLGLETLKITDFQLHASTVKRYGLGAHRGRLNIQAGINENDFYDGAWCAGRN
DLQQWIEVDARRLTRFTGVITQGRNSLWLSDWVTSYKVMVSNDSTWVTVKNGSGDMIFEGNS
EKEIPVLNELPVPMVARYIRINPQSWFDNGSICMRMEILGCPLPDPNNYYHRRNEMTTTDDL
FKHHNYKEMRQLMKVVNEMCPNITRIYNIGKSHQGLKLYAVEISDHPGEHEVGEPEFHYIAGA
HGNEVLGRELLLLLVQFVCQEYLARNARIVHLVEETRIHVLPSLNPBGYEKAYEGGSELGGWS
LGRWTHDGDIDINNNFPDLNTLLWEAEDRQNVPRKVPNHYIAIPEWFLSENATVAAETRAVIAW
MEKIPFVLGGNLQGGELVVAYPYDLVRSPWKTQEHTPTPDDHVFRWLAYSASTHRLMTDARR
RVCHTEDFQKEEGTVNGASWHTVAGSLNDFSYLHTNCFELSIYVGCDKYPHESQLPEEWENNR
ESLIVFMEQVHRGIKGLVRDSHGKGIPNAIISVEGINHDIRTANDGDYWRLNPGEYVVTAKA
EGFTASTKNCMVGYDMGATRCDFTLSKTNMARIREIMEKFGKQPVSLPARRLKLGRKRRQRG

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FIGURE 393

GTCCACATCTCTGCTCAACTGGGTGAGTCCCTCTTAGACCAGCTCTTGTCCATCATTTGCTGAAGTGGACCAAC
TAGTTCCCCAGTAGGGGGTCTCCCTGGCAATTCTTGATCGGCGTTTGGACATCTCAGATCGCTTCCAATGAAGA
TGGCCTTGCTTGGGGTCTGCTGTTTCATAATCATCTAACTATGGGACAAGGTTGTGCCGGCAGCTCTGGGGG
AAGGAGCACGGGGCTGATCAAGCCATCCAGGAAACACTGGAGGACTTGTCCAGCCTTGAAAGAACTCTAGTGGTT
TCTGAATCTAGCCCACTTGGCGGTAAGCATGATGCAACTTCTGCAACTTCTGCTGGGGCTTTTGGGGCCAGGTGG
CTACTTATTTCTTTTAGGGGATTGTCAGGAGGTGACCACTCTCACGGTGAAATACCAAGTGTGAGAGGAAGTGCC
ATCTGGTACAGTGATCGGGAAGCTGTCCAGGAACTGGGCCGGGAGGAGAGGCGGAGGCAAGCTGGGGCCGCTT
CCAGGTGTTGCAGCTGCCTCAGGCGCTCCCCATTAGGTGGACTCTGAGGAAGGCTTGCTCAGCACAGGCAGGCG
GCTGGATCGAGAGCAGCTGTGCCGACAGTGGGATCCCTGCCTGGTTTCCCTTTGATGTGCTTGCCACAGGGGATT
GGCTCTGATCCATGTGGAGATCCAAGTGTGGACATCAATGACCACCAGCCACGGTTTCCCAAAGGCGAGCAGGA
GCTGGAAATCTCTGAGAGCGCTCTCTGCGAACCCGGATCCCCCTGGACAGAGCTCTTGACCCAGACACAGGCC
TAACACCCTGCACACCTACACTCTGTCTCCAGTGAGCACTTTGCCCTGGATGTCATTGTGGGCCCTGATGAGAC
CAAACATGCAGAACTCATAGTGGTGAAGGAGCTGGACAGGGAAATCCATTCATTTTTTGATCTGGTGTAACTGC
CTATGACAATGGGAACCCCCCAAGTCAGGTACCAGCTTGGTCAAGGTCAACGTCTTGAGACTCCAATGACAATAG
CCCTGCGTTTGTGAGAGTTCAGTGGCACTGGAAATCCAAGAAAGATGCTGCACCTGGTACGCTTCTCATAAAAC
GACCGCCACAGACCTGACCAAGGCCCAATGGGGAGGTGGAGTTCTTCCTCAGTAAGCACATGCCTCCAGAGGT
GCTGGACACCTTCAGTATTGATGCCAAGACAGGCCAGGTCACTTCTGCGTCGACCTCTAGACTATGAAAAGAACC
TGCCTACGAGGTGGATGTTGAGGCAAGGGACCTGGGTCCCAATCCTATCCCAGCCATTGCAAAGTTCTCATCAA
GGTCTGGATGTCAATGACAACATCCCAAGCATCCACGTACATGGGCCTCCAGCCATCACTGGTGTGAGAAGC
TCTTCCCAAGGACAGTTTATTGCTCTTGTGATGGCAGATGACTTGGATTGAGGACACAATGGTTTGGTCCACTG
CTGGCTGAGCCAAGAGCTGGGCCACTTCAGGTGAAAAGAACTAATGGCAACACATACATGTTTGCTAACCAATGC
CACACTGGACAGAGAGCAGTGGCCCAATATACCCTCACTCTGTTAGCCCAAGACCAAGGACTCCAGCCCTTATC
AGCCAAGAAACAGCTCAGCATTGAGATCAGTGACATCAACGACAATGCACCTGTGTTTGAGAAAAGCAGGTATGA
AGTCTCCACGCGGGAAAACAACCTTACCCTCTCTTACCTCATTACCATCAAGGCTCATGATGCAGACTTGGGCAT
TAATGGAAAAGTCTCATACCGCATCCAGGACTCCCCAGTTGCTCACTTAGTAGCTATTGACTCCAACACAGGAGA
GGTCACTGCTCAGAGGTCACTGAACATGAAAGATGGCCGGCTTTGAGTTCCAGGTGATCGCAGAGGACAGCGG
GCAACCCATGCTTGATCCAGTGTCTGTGTGGGTGAGCCTCTTGGATGCCAATGATAATGCCCCAGAGGTGGT
CCAGCCTGTGCTCAGCGATGGAAAAGCCAGCCTCTCCGTGCTTGTGAATGCCTCCACAGGCCACCTGCTGGTGCC
CATCGAGACTCCCAATGGCTTGGGCCAGCGGGCACTGACACACCTCCACTGGCCACTCACAGCTCCCGGCCATT
CCTTTTGACAACCATTTGTGGCAAGAGATGCAGACTCGGGGGCAAATGGAGAGCCCCCTCTACAGCATCCGCAATGG
AAATGAAGCCCACCTCTTCATCTCAACCCTCATACGGGGCAGCTGTTCTGTCATGTACCAATGCCAGCAGCCT
CATTGGGAGTGAGTGGGAGCTGGAGATAGTAGAGGACAGGGAAGCCCCCTTACAGACCCGAGCCCTGTT
GAGGGTCACTGTTTGTCAACAGTGTGGACCACCTGAGGGACTCAGCCCGCAAGCCTGGGGCCTTGAGCATGTGAT
GCTGACGGTGTCTGCCTGGCTGTACTGTTGGGCATCTTGGGTTGATCCTGGCTTTGTTTATGTCCATCTGCCG
GACAGAAAAGAAGGACAACAGGGCCTACAACCTGTGCGGAGGCGGAGTCCACCTACCGCCAGCAGCCCAAGAGGCC
CCAGAAACACATTGAGAAGGCAGACATCCACCTCGTGCCTGTGCTCAGGGGTGAGGCAGGTGAGCCTTGTGAAGT
CGGGCAGTCCCACAAGATGTGGACAAGGAGGCGATGATGGAAGCAGGCTGGGACCCCTGCCTGCAGGCCCCCTT
CCACCTCACCCCGACCTGTACAGGACGCTGCGTAATCAAGGCAACCCAGGGAGCACCGGCGGAGAGCCGAGGT
GCTGCAAGACACGGTCAACCTCCTTTTCAACCATCCAGGCAGAGGAATGCCTCCCGGGAGAACCTGAACCTTCC
CGAGCCCCAGCCTGCCACAGGCCAGCCACGTTCCAGGCCTCTGAAGGTTGCAGGCAGCCCCACAGGGAGGCTGGC
TGGAGACCAGGGCAGTGAGGAAGCCCCACAGAGGCCACCAGCCTCCTCTGCAACCCTGAGACGGCAGCGACATCT
CAATGGCAAAGTGTCCCCTGAGAAAAGATCAGGGCCCCGTGAGATCCTGCGGAGCCTGGTCCGGCTGTCTGTGGC
TGCCTTTCGCGAGCGGAACCCCGTGGAGGAGCTCACTGTGGATTCTCCTCCTGTTTACGAAATCTCCAGCTGCT
GTCCTTGCTGCATCAGGGCCAATTCCAGCCCAAACCAACCCAGGAGAAATAAGTACTTGGCCCAAGCCAGGAGG
CAGCAGGAGTGCAATCCAGACACAGATGGCCCAAGTGCAAGGGCTGGAGGCCAGACAGACCCAGAACAGGAGGA
AGGGCCTTTGGATCCTGAAGAGGACCTCTCTGTGAAGCAACTGCTAGAAGAAGAGCTGTCAAGTCTGCTGGACCC
CAGCACAGGTCTGGCCCTGGACCGGCTGAGCGCCCTGACCCGGCCTGGATGGCGAGACTCTCTTTGCCCTCAC
CACCAACTACCGTGACAATGTGATCTCCCCGGATGCTGCAGCCACGGAGGAGCCGAGGACCTTCCAGACGTTCCG
CAAGGCAGAGGCACAGAGCTGAGCCCAACAGGCACGAGGCTGGCCAGCACCTTTGCTCGGAGATGAGTCACT
GCTGGAGATGCTGCTGGAACAGCGCTCCAGCATGCCGTGGAGCCGCTCCGAGGCGCTCCGAGGCGCTCTCGGT
CTGCGGGAGGACCTCAGTTTAGACTTGGCCACCAGTGCAGCCTCAGGCATGAAAGTGCAAGGGGACCCAGGTGG
AAAGACGGGGACTGAGGGCAAGAGCAGAGGCAGCAGCAGCAGCAGCAGGTCCTGTGAACATACCTCAGACGCCT
CTGGATCCAAGAACCAGGGGCTGAGGATCTGTGGACAAGAGCTGGTTTCTAAAATCTTGTAACTCACTAGCTAG
CGGCGGCTGAGAATTTAGGGTGACTGATGCTACCCCCACAGAGGAGGCAAGAGCCCCAGGACTAACAGCTGAC
TGACCAAAGCAGCCCTTGTAAAGCAGCTCTGAGTCTTTTGGAGGACAGGGACGGTTTGTGGCTGAGATAAGTGT
TCCTGGCAAAACATATGTGGAGCACAAGGGTCAGTCTCTGGCAGAACAGATGCCACGGAGTATCACAGGCAGG
AAAGGTTGGCCTTCTTGGGTGAGGAGTCAGGGGCTGTACCCTGGGGGTGCCAGGAAATGCTCTCTGACCTAT
CAATAAGGAAAAGCAGTAAAAAAAAAAAAAAAAAAAAA

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FIGURE 394

MMQLLQLLLGLLGPGGYLFLLGDCQEVTTLTVKYQVSEEVPSGTVIGKLSQELGREERRRQAG
 AAFQVLQLPQALPIQVDSEEGLLSTGRRLDREQLCRQWDPCLVSFDVLATGDLALIHVEIQVL
 DINDHQPRFPKGEQELEISESASLRTRIPLDRALDPDTGPNTLHTYTLSPSEHFALDVIVGPD
 ETKHAELIVVKELDREIHSFFDLVLTAYDNGNPPKSGTSLVKVNVLDSDNDNSPAFAESSLALE
 IQEDAAPGTTLLIKLTATDPDQGPNGEVEFFLSKHMPPEVLDTFSIDAKTGQVILRRPLDYEKN
 PAYEVDVQARDLGPNPIPAHCKVLIKVLVDVNDNIPSIHVTWASQPSLVSEALPKDSFIALVMA
 DDLDSGHNGLVHCWLSQELGHFRLKRTNGNTYMLLTNATLDREQWPKYTLTLLAQDQGLQPLS
 AKKQLSIQISDINDNAPVFEKSRYEVSTRENNLPSLHLITIKAHDADLGINGKVSRYRIQDSPV
 AHLVAIDSNTGEVTAQRSLNYEEMAGFEFQVIAEDSGQPMLASSVSVVWVSLLDANDNAPEVVQ
 PVLSDGKASLSVLVNASTGHLLVPIETPNGLGPAGTDTPLATHSSRPFLTTIVARDADSGA
 NGEPLYSIRNGNEAHLFILNPHTGQLFVNVTNASSLIGSEWELEIIVVEDQGSPPLQTRALLRV
 MFVTSVDHLRDSARKPGALSMSMLTVICLAVLLGIFGLILALFMSICRTEKKDNRAYNCREAE
 STYRQQPKRPQKHQKADIHLVPVLRGQAGEPCEVGQSHKDVDKEAMMEAGWDPCQLQAPFHLT
 PTLYRTLNRNQGNGAPAESREVLQDTVNLLFNHPRQRNASRENLNLPQPATGQPRSRPLKV
 AGSPTGRLAGDQGSEEAPQRPPASSATLRRQRHLNGKVSPEKESGPRQILRSLVRLSVAFAE
 RNPVEELTVDSPPVQQISQLLSLLHQGFQPKPNHRGNKYLAKEGGSRSAPDPTDGPSARAGG
 QTDPEQEEGPLDPEEDLSVKQLLEEELSSLLDPSTGLALDRLSAPDPAWMARLSLPLTTNYRD
 NVISPDAAATEEPRTFQTFGKAEAPELSPTGTRLASTFVSEMSSLLEMLLEQRSSMPVEAASE
 ALRRLSVCGRTLSLDDLATSAASGMKVQGDPPGGKTGTEGKSRGSSSSSRCL

Important features:**Signal peptide:**

amino acids 1-13

Transmembrane domain:

amino acids 719-739

N-glycosylation site.

amino acids 415-418, 582-585, 659-662, 662-665 and 857-860

Cadherins extracellular repeated domain signature.

amino acids 123-133, 232-242, 340-350, 448-458 and 553-563

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FIGURE 395

CCCAGGCTCTAGTGCAGGAGGAGAAGGAGGAGGAGCAGGAGGTGGAGATTCCCAGTTAAAAGG
CTCCAGAATCGTGTACCAGGCAGAGAACTGAAGTACTGGGGCCTCCTCCACTGGGTCCGAATC
AGTAGGTGACCCCGCCCCTGGATTCTGGAAGACCTCACCATGGGACGCCCCCGACCTCGTGCG
GCCAAGACGTGGATGTTCTGCTCTTGCTGGGGGGAGCCTGGGCAGGACACTCCAGGGCACAG
GAGGACAAGGTGCTGGGGGGTCATGAGTGCCAACCCCATTCGCAGCCTTGGCAGGCGGCCTTG
TTCCAGGGCCAGCAACTACTCTGTGGCGGTGTCCTTGTAGGTGGCAACTGGGTCCTTACAGCT
GGCCACTGTAAAAAACCGAAATACACAGTACGCCTGGGAGACCACAGCCTACAGAATAAAGAT
GGCCCAGAGCAAGAAATACCTGTGGTTCAGTCCATCCCACACCCCTGCTACAACAGCAGCGAT
GTGGAGGACCACAACCATGATCTGATGCTTCTTCAACTGCGTGACCAGGCATCCCTGGGGTCC
AAAGTGAAGCCCATCAGCCTGGCAGATCATTGCACCCAGCCTGGCCAGAAGTGCACCGTCTCA
GGCTGGGGCACTGTCACCAGTCCCCGAGAGAATTTTCCTGACACTCTCAACTGTGCAGAAGTA
AAAATCTTTCCCCAGAAGAAGTGTGAGGATGCTTACCCGGGGCAGATCACAGATGGCATGGTC
TGTGCAGGCAGCAGCAAAGGGGCTGACACGTGCCAGGGCGATTCTGGAGGCCCCCTGGTGTGT
GATGGTGCCTCCAGGGCATCACATCCTGGGGCTCAGACCCCTGTGGGAGGTCCGACAAACCT
GGCGTCTATACCAACATCTGCCGCTACCTGGACTGGATCAAGAAGATCATAGGCAGCAAGGGC
TGATTCTAGGATAAGCACTAGATCTCCCTTAATAAACTCACAACTCTCTGGTTC

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FIGURE 396

MGRPRPRAAKTWMFLLLLGGAWAGHSRAQEDKVLGGHECQPHSQPWQAALFQGQQLLCGGVLV
GGNWVLTAAHCKKPKYTVRLGDHSLQNKDGPEQEIPVVQSIPHPCYNSSDVEDHNHDLMLLQL
RDQASLGSKVKPISLADHCTQPGQKCTVSGWGTVTSPRENFDTLNCAEVKIFPQKKCEDAYP
GQITDGMVCAGSSKGADTCQGDSSGGLVCDGALQGITSWGSDPCGRSDKPGVYTNICRYLDWI
KKIIGSKG

Important Features:**Signal peptide:**

amino acids 1-23

Transmembrane domain:

amino acids 51-71

N-glycosylation site.

amino acids 110-113

Serine proteases, trypsin family, histidine active site.

amino acids 69-74 and 207-217

Tyrosine kinase phosphorylation site.

amino acids 182-188

Kringle domain proteins motif

amino acids 205-217

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FIGURE 397

GGCGGCTGCTGAGCTGCCTTGAGGTGCAGTGTTGGGGATCCAGAGCCATGTCGGACCTGCTAC
TACTGGGCCTGATTGGGGGCCTGACTCTCTTACTGCTGCTGACGCTGCTGGCCTTTGCCGGGT
ACTCAGGGCTACTGGCTGGGGTGGAAGTGAGTGCTGGGTACCCCCCATCCGCAACGTCACTG
TGGCCTACAAGTTCCACATGGGGCTCTATGGTGAGACTGGGCGGCTTTTCACTGAGAGCTGCA
GCATCTCTCCCAAGCTCCGCTCCATCGCTGTCTACTATGACAACCCCCACATGGTGCCCCCTG
ATAAGTGCCGATGTGCCGTGGGCAGCATCCTGAGTGAAGGTGAGGAATCGCCCTCCCCTGAGC
TCATCGACCTCTACCAGAAATTTGGCTTCAAGGTGTTCTCCTTCCCGGCACCCAGCCATGTGG
TGACAGCCACCTTCCCCTACACCACCATTTCTGTCCATCTGGCTGGCTACCCGCCGTGTCCATC
CTGCCTTGGACACCTACATCAAGGAGCGGAAGCTGTGTGCCTATCCTCGGCTGGAGATCTACC
AGGAAGACCAGATCCATTTTCATGTGCCCACTGGCACGGCAGGGAGACTTCTATGTGCCTGAGA
TGAAGGAGACAGAGTGGAATGGCGGGGGCTTGTGGAGGCCATTGACACCCAGGTGGATGGCA
CAGGAGCTGACACAATGAGTGACACGAGTTCTGTAAGCTTGGGAAGTGAGCCCTGGCAGCCGGG
AGACTTCAGCTGCCACACTGTACCTGGGGCGAGCAGCCGTGGCTGGGATGACGGTGACACCC
GCAGCGAGCACAGCTACAGCGAGTCAGGTGCCAGCGGCTCCTCTTTTGAGGAGCTGGACTTGG
AGGGCGAGGGGGCCCTTAGGGGAGTCACGGCTGGACCTGGGACTGAGCCCCTGGGGACTACCA
AGTGGCTCTGGGAGCCCACTGCCCCTGAGAAGGGCAAGGAGTAACCCATGGCCTGCACCCTCC
TGCAGTGACAGTTGCTGAGGAACTGAGCAGACTCTCCAGCAGACTCTCCAGCCCTCTTCCTCCT
TCCTCTGGGGGAGGAGGGGTTCTGAGGGACCTGACTTCCCCTGCTCCAGGCCTCTTGCTAAG
CCTTCTCCTCACTGCCCTTTAGGCTCCCAGGGCCAGAGGAGCCAGGGACTATTTTCTGCACCA
GCCCCAGGGCTGCCGCCCTGTTGTGTCTTTTTTTTCAGACTCACAGTGAGCTTCCAGGACC
CAGAATAAAGCCAATGATTTACTTGTTTACCTGGAAAAAAAAAAAAAAAAA

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FIGURE 398

MSDLLLLGLIGGLTLLLLLTLLAFAGYSGLLAGVEVSAGSPPIRNVTVAYKFHMGLYGETGRL
FTESCSISPKLRSIAYYYDNPHMVPPDKCRCAVGSILSEGEESPSPELIDLYQKFGFKVFSFP
APSHVVTATFPYTTILSIWLATTRVHPALDITYIKERKLCAYPRLEIYQEDQIHMCPLARQGD
FYVPEMKETEWKWRGLVEAIDTQVDGTGADTMSDTSSVSLEVSPGSRETSAA TLSPGASSRGW
DDGDTRSEHSYSESGASGSSFEELDLEGEGLGESRLDPGTEPLGTTKWLWEPTAPEKGKE

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FIGURE 400

MSNSVPLLCFWSLCYCFAAGSPVPFGPEGRLEDKLHKPKATQTEVKPSVRFNLRITSKDPEHEG
CYLSVGHSQPLEDCSFNMTAKTFFIIHGWTMSGIFENWLHKLVSALHTREKDANVVVVDWLPL
AHQLYTDAVNNTRVVGHSIARMLDWLQEKDDFSLGNVHLIGYSLGAHVAGYAGNFVKGTVGRI
TGLDPAGPMFEGADIAHKRLSPDDADFVDVLHTYTRSEGLSIGIQMPVGHIDIYPNGGDFQPGC
GLNDVLGSIAYGTITEVVKCEHERAVHLFVDSLQNQDKPSFAFQCTDSNRFKKGICLSCRKNR
CNSIGYNACKMRNKRNSKMYLKTRAGMPFRGNLQSLECP

Important features:**Signal peptide:**

amino acids 1-16

Lipases, serine active site.

amino acids 163-172

N-glycosylation sites.

amino acids 80-83 and 136-139

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FIGURE 401

CTTCCCAGCCCTGTGCCCCAAAGCACCTGGAGCATATAGCCTTGCAGAACTTCTACTTGCCTG
CCTCCCTGCCTCTGGCC**ATG**GCCTGCCGGTGCCTCAGCTTCCTTCTGATGGGGACCTTCCTGT
CAGTTTCCCAGACAGTCCTGGCCCAGCTGGATGCACTGCTGGTCTTCCCAGGCCAAGTGGCTC
AACTCTCCTGCACGCTCAGCCCCAGCACGTCACCATCAGGGACTACGGTGTGTCCTGGTACC
AGCAGCGGGCAGGCAGTGCCCCCTCGATATCTCCTCTACTACCGCTCGGAGGAGGATCACCACC
GGCCTGCTGACATCCCCGATCGATTCTCGGCAGCCAAGGATGAGGCCCACAATGCCTGTGTCC
TCACCATTAGTCCCGTGCAGCCTGAAGACGACGCGGATTACTACTGCTCTGTTGGCTACGGCT
TTAGTCCC**TAG**GGGTGGGGTGTGAGATGGGTGCCTCCCCTCTGCCTCCCATTCTGCCCTGA
CCTTGGGTCCCTTTTAAACTTTCTCTGAGCCTTGCTTCCCCTCTGTAAAATGGGTTAATAATA
TTCAACATGTCAACAAC

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FIGURE 402

MACRCLSFLLMGTFLSVSQTVLAQLDALLVFPGQVAQLSCTLSPQHVTIRDYGVSWYQQRAGS
APRYLLYYRSEEDHHRPADIPDRFSAKDEAHNACVLTISPVQPEDDADYYCSVGYGFSF

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FIGURE 403

CGCGCCGGGCGCAGGGAGCTGAGTGGACGGCTCGAGACGGCGGCGCGTGCAGCAGCTCCAGAAAGCAGCGAGTTG
GCAGAGCAGGGCTGCATTTCCAGCAGGAGCTGCGAGCACAGTGCTGGCTCACAACAAGATGCTCAAGGTGTCAGC
CGTACTGTGTGTGTGTGCAGCCGCTTGGTGCAGTCAGTCTCTCGCAGCTGCCGCGGCGGTGGCTGCAGCCGGGGG
GCGGTCCGACGGCGGTAATTTTCTGGATGATAAACAATGGCTCACCACAATCTCTCAGTATGACAAGGAAGTCGG
ACAGTGGAACAAATTCGAGACGAAGTAGAGGATGATTATTTCCGCACTTGGAGTCCAGGAAAACCTTCGATCA
GGCTTTAGATCCAGCTAAGGATCCATGCTTAAAGATGAAATGTAGTCGCCATAAAGTATGCATTGCTCAAGATTC
TCAGACTGCAGTCTGCATTAGTCACCGGAGGCTTACACACAGGATGAAAGAAGCAGGAGTAGACCATAGGCAGTG
GAGGGGTCCCATATTATCCACCTGCAAGCAGTGCCCAGTGGTCTATCCCAGCCCTGTTTGTGGTTCAGATGGTCA
TACCTACTCTTTTCAGTGCAAACCTAGAATATCAGGCATGTGTCTTAGGAAAACAGATCTCAGTCAAATGTGAAGG
ACATTGCCCATGTCTTCAGATAAGCCCACCAGTACAAGCAGAAATGTTAAGAGAGCATGCAGTGACCTGGAGTT
CAGGGAAGTGGCAAACAGATTGCGGGACTGGTTCAAGGCCCTTCATGAAAGTGGAAGTCAAAACAAGAAGACAAA
AACATTGCTGAGGCCTGAGAGAAGCAGATTCGATACCAGCATCTTGCCAATTTGCAAGGACTCACTTGGCTGGAT
GTTTAACAGACTTGATACAACTATGACCTGCTATTGGACCAGTCAGAGCTCAGAAGCATTTACCTTGATAAGAA
TGAACAGTGTAACAAGGCATTCTTCAATTCTTGTGACACATACAAGGACAGTTTAATATCTAATAATGAGTGGTG
CTACTGCTTCCAGAGACAGCAAGACCCACCTTGCCAGACTGAGCTCAGCAATATTGAGAAGCGGCAAGGGGTAAA
GAAGCTCCTAGGACAGTATATCCCCCTGTGTGATGAAGATGGTTACTACAAGCCAACACAATGTCATGGCAGTGT
TGGACAGTGCTGGTGTGTTGACAGATATGGAAATGAAGTCATGGGATCCAGAATAAATGGTGTTCAGATTGTGC
TATAGATTTTGAGATCTCCGGAGATTTTGCTAGTGGCGATTTTCATGAATGGACTGATGATGAGGATGATGAAGA
CGATATTATGAATGATGAAGATGAAATTGAAGATGATGATGAAGATGAAGGGGATGATGATGATGGTGGTGTGA
CCATGATGTATACATTTGATTGATGACAGTTGAAATCAATAAATTCTACATTTCTAATATTTACAAAAATGATAG
CCTATTTAAATTATCTTCTTCCCCAATAACAAAATGATTCTAAACCTCACATATATTTGTATAATTATTTGAA
AAATTGCAGCTAAAGTTATAGAACTTTATGTTTAAATAAGAATCATTTGCTTTGAGTTTTTATATTCCTTACACA
AAAAGAAAATACATATGCAGTCTAGTCAGACAAAATAAAGTTTTGAAGTGCTACTATAATAAATTTTTTACGAGA
ACAACTTTGTAAATCTTCATAAGCAAAATGACAGCTAGTGCTTGGGATCGTACATGTTAATTTTTTTGAAAGAT
AATTCTAAGTGAAATTTAAATAAATAAATTTTTAATGACCTGGGTCTTAAGGATTTAGGAAAAATATGCATGCT
TTAATTGCATTTCCAAAGTAGCATCTTGCTAGACCTAGATGAGTCAGGATAACAGAGAGATACCACATGACTCCA
AAAAAAAAAAAAA

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FIGURE 404

MLKVSAVLCVCAAAWCSQSLAAAAVAAAGGRSDGGNFLDDKQWLTTISQYDKEVGQWNKFRD
EVEDDYFRTWSPGKPFQALDPAKDPCLMKCSRHKVCIAQDSQTAVCISHRRLTHRMKEAGV
DHRQWRGPILSTCKQCPVVYPSPVCGSDGHTYSFQCKLEYQACVLGKQISVKCEGHCPSPDK
PTSTSRNVKRACSDLEFREVANRLRDWFKALHESGSQNKKTKTLLRPERSRFDTSILPICKDS
LGWMFNRLDTNYDLLLDQSELRSIYLDKNEQCTKAFFNSCDTYKDSLISNNEWCYCFQRQQDP
PCQTELSNIQKRQGVKKLLGQYIPLCDEDGYKPTQCHGSGVQCWCVDRYGNEVMGSRINGVA
DCAIDFEISGDFASGDFHEWTDDEDEDDIMNDEDEIEDDDDEDEGDDDDGGDDHDVYI

Important features:**Signal peptide:**

amino acids 1-16

Leucine zipper pattern.

amino acids 246-267

N-myristoylation sites.

amino acids 357-362, 371-376 and 376-381

Thyroglobulin type-1 repeat proteins

amino acids 353-365 and 339-352

FIGURE 405

[illegible]

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FIGURE 406

MTPQSLLQTTLFLLSLLFLVQGAHGRGHREDFRFC SQRNQTHRSSLHYKPTPDLRISIENSEE
ALTVHAPFPAAHPASRSFPDPRGLYHFCLYWNRHAGRLHLLYGKRDFLLSDKASSLLCFQHQE
ESLAQGPPLLATSVTSWWSPQNI SLPSAASF TFSFHSPHTAAHNASVDMCELKRDLQLLSQF
LKHPQKASRRPSAAPASQQ LQSLESKLTSVRFMGDMVSFEEDRINATVWKLQPTAGLQDLHIH
SRQEEEQSEIMEYSVLLPRTL FQRTKGRSGEAEKRLLLVD FSSQALFQDNSSQVLGEKVLGI
VVQNTKVANLTEPVVLT FQHQLQPKNVT LQCVFWVEDPTLSSPGHWSSAGCETVRRETQTSCF
CNHLTYFAVLMVSSVEVD AVHKHYLSLLSYVGCVV SALACLVTIAAYLCSRVP LPCR RKPRDY
TIKVHMNLLLA VFLLDTSFLLSEPVALTGSEAGCRASAI FLHFSLLTCLSWMGLEGYNLYRLV
VEVFGTYVPGYLLKLSAMGWGFPIFLVTLVALVDVDNYGPIILAVHRTPEGVIYPSMCWIRDS
LVSYITNLGLFSLVFLFN MAMLATMVVQILRLRPHTQKWSHVL TLLGLSLVLGLPWALIFFSF
ASGTFQLVVLVLYLFSIITSFQGF LIFIWWSMRLQARGGPSPLKSNSDSARLP ISSGSTSSSRI

Important features:**Signal peptide:**

amino acids 1-25

Putative transmembrane domains:amino acids 382-398, 402-420, 445-468, 473-491, 519-537, 568-590
and 634-657**Microbodies C-terminal targeting signal.**

amino acids 691-693

cAMP- and cGMP-dependent protein kinase phosphorylation sites.

amino acids 198-201 and 370-373

N-glycosylation sites.amino acids 39-42, 148-151, 171-174, 234-237, 303-306, 324-327
and 341-344**G-protein coupled receptors family 2 proteins**

amino acids 475-504

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FIGURE 407

TTGTGACTAAAAGCTGGCCTAGCAGGCCAGGGAGTGCAGCTGCAGGCGTGGGGGTGGCAGGAG
CCGCAGAGCCAGAGCAGACAGCCGAGAAACAGGTGGACAGTGTGAAAGAACCAGTGGTCTCGC
TCTGTTGCCCAGGCTAGAGTGTACTGGCGTGATCATAGCTCACTGCAGCCTCAGACTCCTGGA
CTTGAGAAATCCTCCTGCCTTAGCCTCCTGCATATCTGGGACTCCAGGGGTGCACTCAAGCCC
TGTTTCTTCTCCTTCTGTGAGTGGACCACGGAGGCTGGTGAGCTGCCTGTCATCCCAAAGCTC
AGCTCTGAGCCAGAGTGGTGGTGGCTCCACCTCTGCCGCCGGCATAGAAGCCAGGAGCAGGGC
TCTCAGAAGGCGGTGGTGCCCAGCTGGGATCATGTGTTGGCCCTGGTCTGTCTGCTCAGCTG
CCTGCTACCCTCCAGTGAGGCCAAGCTCTACGGTCGTTGTGAACTGGCCAGAGTGCTACATGA
CTTCGGGCTGGACGGATACCGGGGATACAGCCTGGCTGACTGGGTCTGCCTTGCTTATTTTAC
AAGCGGTTTCAACGCAGCTGCTTTGGACTACGAGGCTGATGGGAGCACCAACAACGGGATCTT
CCAGATCAACAGCCGGAGGTGGTGCAGCAACCTCACCCCGAACGTCCCCAACGTGTGCCGGAT
GTACTGCTCAGATTTGTTGAATCCTAATCTCAAGGATACCGTTATCTGTGCCATGAAGATAAC
CCAAGAGCCTCAGGGTCTGGGTACTGGGAGGCCTGGAGGCATCACTGCCAGGGAAAAGACCT
CACTGAATGGGTGGATGGCTGTGACTTCTAGGATGGACGGAACCATGCACAGCAGGCTGGGAA
ATGTGGTTTGGTTCCTGACCTAGGCTTGGGAAGACAAGCCAGCGAATAAAGGATGGTTGAACG
TGAAA

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FIGURE 408

MLLALVCLLSCLLPSSSEAKLYGRCELARVLHDFGLDGYRGYSLADWVCLAYFTSGFNAAALDY
EADGSTNNGIFQINSRRWCSNLTPNVPNVCRMYSDDLNP NLKDTVICAMKITQEPQGLGYWE
AWRHHCQGKDLTEWVDGCDF

Important features:**Signal peptide:**

amino acids 1-18

N-myristoylation site.

amino acids 67-72

Homologous region to Alpha-lactalbumin / lysozyme C proteins.

amino acids 34-58 (catalytic domain), 111-132 and 66-107

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FIGURE 409

CAGACTCCAGATTTCCCTGTCAACCACGAGGAGTCCAGAGAGGAAACGCGGAGCGGAGACAAACAGTACCTGACGC
CTCTTTTCAGCCCCGGGATCGCCCCAGCAGGG~~ATG~~GGCGACAAGATCTGGCTGCCCTTCCCCGTGCTCCTTCTGGCC
GCTCTGCCTCCGGTGCTGCTGCCTGGGCGGCCGGCTTCACACCTTCCCTCGATAGCGACTTCACCTTTACCCTT
CCCCCGCGCCAGAAAGGAGTGCTTCTACCAGCCCATGCCCTGAAGGCCTCGCTGGAGATCGAGTACCAAGTTTTA
GATGGAGCAGGATTAGATATTGATTTCCATCTTGCTCTCCAGAAGGCAAACCTTAGTTTTTGAACAAAGAAAA
TCAGATGGAGTTCACACTGTAGAGACTGAAGTTGGTGATTACATGTTCTGCTTTGACAATACATTCAGCACCATT
TCTGAGAAGGTGATTTTCTTTGAATTAATCCTGGATAATATGGGAGAACAGGCACAAGAACAAGAAGATTGGAAG
AAATATATTACTGGCACAGATATATTGGATATGAACTGGAAGACATCCTGGAATCCATCAACAGCATCAAGTCC
AGACTAAGCAAAAGTGGGCACATACAAATTCTGCTTAGAGCATTGAAGCTCGTGATCGAAACATACAAGAAAGC
AACTTTGATAGAGTCAATTTCTGGTCTATGGTTAATTTAGTGGTTCATGGTGGTGGTGTGAGCCATTCAAGTTTAT
ATGCTGAAGAGTCTGTTTGAAGATAAGAGGAAAAGTAGAACT~~TAA~~AACTCCAACTAGAGTACGTAACATTGAAA
AATGAGGCATAAAAAATGCAATAAACTGTTACAGTCAAGACCATTAATGGTCTTCTCCAAAATATTTTGAGATATA
AAAGTAGGAAACAGGTATAATTTTAATGTGAAAATTAAGTCTTCACCTTCTGTGCAAGTAATCCTGCTGATCCAG
TTGTACTTAAGTGTTAACAGGAATATTTTGCAGAATATAGGTTTAACTGAATGAAGCCATATTAATAACTGCAT
TTTCCTAACTTTGAAAAATTTTGCAAATGTCTTAGGTGATTTAAATAAATGAGTATTGGGCCTAATTGCAACACC
AGTCTGTTTTTAAACAGGTTCTATTACCCAGAATTTTTTGTAAATGCGGCAGTTACAAATTAAGTGTGGAAGTTT
TCAGTTTTAAGTTATAAATCACCTGAGAATTACCTAATGATGGATTGAATAAATCTTTAGACTACAAAAGCCCAA
CTTTTCTCTATTTACATATGCATCTCTCCTATAATGTAAATAGAATAATAGCTTTGAAATACAATTAGGTTTTTG
AGATTTTTTATAACCAATACATTTTCAGTGTAACATATTAGCAGAAAGCATTAGTCTTTGTACTTTGCTTACATTC
CCAAAAGCTGACATTTTACGATTCTTAAAAACACAAGTTACACTTACTAAAATTAGGACATGTTTTCTCTTTG
AAATGAAGAATATAGTTTAAAGCTTCTCCTCCATAGGGACACATTTTCTCTAACCTTAACTAAAGTGTAGGA
TTTTAAAATTAATGTGAGGTAAAATAAGTTTTATTTTAATAGTATCTGTCAAGTTAATATCTGTCAACAGTTAA
TAATCATGTTATGTTAATTTTAACATGATTGCTGACTTGGATAATTCATTATTACCAGCAGTTATGAAGGAAATA
TTGCTAAAATGATCTGGGCCTACCATAAATAAATATCTCCTTTTCTGAGCTCTAAGAATTATCAGAAAACAGGAA
AGAATTTAGAAAACTTGAGAAAACCTAATCCAAAATAAAATTCACCTAAGTAGAACTATAAATAAATATCTAGA
ATCTGACTGGCTCATCATGACATCCTACTCATAACATAAATCAAAGGAGATGATTAATTTCCAGTTAGCTGGAAG
AACTTTGGCTGTAGGTTTTTATTTTCTACAAGAATTCTGGTTGAATTATTTTTGTAAAGCAGGTACATTTTATA
AAATGTAAGCCCTACTGTAAGGTTTAGCACTGGGTGTACATATTTATTAATAAATTTTTATTATAACAACTTTTAT
TAAAATGGCCTTTCTGAACACTTTATTTATTGATGTTGAAGTAAGGATTAGAAACATAGACTCCCAAGTTTTAAA
CACCTAAATGTGAATAACCCATATATACAACAAAGTTTCTGCCATCTAGCTTTTTGAAGTCTATGGGGGTCTTAC
TCAAGTACTAGTAATTTAACTTCATCATGAATGAACATAAATTTTTAAGTTATGCCCATTTATAACGTTGTTTAT
GACTACATTGTGAGTTAGAAAACAACTTAAAATTTGGGGTATAGAACCCTCAACAGGTTAGTAATGCTGGAATT
CTTGATGAGCAATAATGATAACCAGAGAGTGATTTCAATTTACACTCATAGTAGTATAAAAAGAGATACATTTCCC
TCTTAGGCCCCCTGGGAGAAGAGCAGCTTAGATTTCCCTACTGGCAAGGTTTTTAAAAATGAGGTAAATGCCGTAT
ATGATCAATTACCTTAATTGGCCAAGAAAATGCTTCAGGTGTCTAGGGGTATCCTCTGCAACACTTGCAGAACAA
AGGTCAATAAGATCCTTGCCATGAATACCCCTCCCTTTTGCGCTGTTAAATTTGCAATGAGAAGCAAAATTTACA
GTACCATAACTAATAAAGCAGGGTACAGATATAAACTACTGCATCTTTTCTATAAACTGTGATTAAGAATTCTA
CCTCTCCTGTATGGCTGTTACTGTACTGTACTCTCTGACTCCTTACCTAACAAATGAATTTGTTACATAATCTTCT
ACATGTATGATTTGTGCCACTGATCTTAAACCTATGATTACAGTAACCTTCTTACCATATAAAAACGATAATTGCTT
TATTTGGAAGAATTTAGGAATACTAAGGACAATTATTTTATAGACAAAGTAAAAGACAGATATTTAAGAGG
CATAACCAAAAAAGCAAACTTGTAAACAGAGTAAAAATCTTAAATATTTCTAAAGACATACTGTTTATCTGCTT
CATATGCTTTTTTTAATTTCACTATTCCATTTCTAAATTAAGTTATGCTAAATTGAGTAAGCTGTTTATCACTT
AACAGCTCATTTTGTCTTTTCAATATACAAATTTTAAAAATACTACAATATTTAACTAAGGCCCAACCGATTTC
CATAATGTAGCAGTTACCGTGTTACCTCACACTAAGGCCTAGAGTTTGCTCTGATATGCATTTGGATGATTAAT
GTTATGCTGTTCTTTTATGTGAATGTCAAGACATGGAGGGTGGTTGTAATTTTATGGTAAAATTAATCCTTCTTA
CACATAATGGTGTCTTAAATTGACAAAAAATGAGCACTTACAATTGTATGTCTCCTCAAATGAAGATTCTTTAT
GTGAAATTTTAAAGACATTGATTCGCGCATGTAAGGATTTTTCATCTGAAGTACAATAATGCACAATCAGTGTTG
CTCAAAGTCTTTTATACTTATAAACAGCCATCTTAAATAAGCAACGTATTGTGAGTACTGATATGTATATAATAA
AAATTATCAAAGGAAAA

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FIGURE 410

MGDKIWLPFPVLLLAALPPVLLPGAAGFTPSLDSDFTFLLPAGQKECFYQPMPLKASLEIEYQ
VLDGAGLDIDFHLASPEGKTLVFEQRKSDGVHTVETEVGDYMFCDNTFSTISEKVIFFELIL
DNMGEQAQEQEDWKKYITGTDILDMKLEDILESINSIKSRLSKSGHIQILLRAFEARDRNIQE
SNFDRVNFWSMVNLVVMVVVSAIQVYMLKSLFEDKRKSRT

Important features:**Signal peptide:**

amino acids 1-23

Transmembrane domain:

amino acids 195-217

N-myristoylation site.

amino acids 43-48

Tyrosine kinase phosphorylation site.

amino acids 55-62

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FIGURE 411

CCCAGCTGAGGAGCCCTGCTCAAGACACGGTCACTGGATCTGAGAACTTCCCAGGGGACCGCATTCAGAGTCA
GTGACTCTGTGAAGCACCCACATCTACCTCTTGCCACGTTCCACGGGCTTGGGGGAAAAGATGCTGGGGACCAAG
GCCTGGGTGTCTCTCTCTGGTCTGGAAGTCACATCTGTGTGGGGAGACAGACGATGCTACCCAGTCAGTA
AGAAGAGTCCAGCCTGGGAAGAAGAACCCACGATCTTTGCCAAGCCTGCCGACACCCCTGGAGAGCCCTGGTGAG
TGGACAACATGGTTCAACATCGACTACCCAGGCGGGGAAGGGCGACTATGAGCGGCTGGAGGCCATTCGCTTCTAC
TATGGGGACCGTGTATGTGCCCGTCCCCTGCGGCTAGAGGCTCGGACCACTGACTGGACACCTGCGGGCAGCACT
GGCCAGGTGGTCCATGGTAGTCCCCGTGAGGGTTTCTGGTGCCTCAACAGGGAGCAGCGGCCTGGCCAGAACTGC
ACCTGCCCAATGGGCCAGGTGAATGCTGACTGTGATGCTGTCGATGTGCCAGGACTTCATGCTTTCATGGGGCTGTC
TCTCCCTGGAGCAAGTGCTCAGCTGCCTGTGGTCACTGGGGTCCAGACTCGCACACGCATTTGCTTGGCAGAG
ATGGTGTGCTGTGCAGTGAGGCCAGCGAAGAGGGTCACTGCTGATGGGCCAGGACTGTACAGCCTGTGACCTG
ACCTGCCCAATGGGCCAGGTGAATGCTGACTGTGATGCTGTCGATGTGCCAGGACTTCATGCTTTCATGGGGCTGTC
TCCCTTCCCGGAGGTGCCCGAGCCTCAGGGGCTGCTATCTACCTCCTGACCAAGACGCCGAAGCTGCTGACCCAG
ACAGACAGTGAATGGGAGATTCCGAATCCCTGGCTTGTGCCCTGATGGCAAAGCATCCTGAAGATCACAAAGGTC
AAGTTTGGCCCATTTGTAATGCTGACCAATGCCAGGAGCCAGCCACCATCAAGGCAGAGTTTGTGAGG
GCAGAGACTCCATACATGGTGTGAACCTGAGACAAAAGCAGGAGAGCTGGGCAGAGCGTGTCTCTGTGCTGT
AAGGCCACAGGGAAGCCAGGCCAGACAAGTATTTTTGGTATCATAATGACACATTGCTGGATCCTTCCCTCTAC
AAGCATGAGAGCAAGCTGGTGTGAGGAACTGCAGCAGCACCAGGCTGGGGAGTACTTTTGAAGGCCCCAGAGT
GATGCTGGGGCTGTGAAGTCCAAGGTTGCCAGCTGATTGTACAGCATCTGATGAGACTCCTTGCAACCCAGTT
CCTGAGAGCTATCTTATCCGGCTGCCCATGATTGCTTTCAGAAATGCCACCAACTCCTTCTACTATGACGTGGGA
CGTGGCCCTGTTAAGACTTGTGCAGGGCAGCAGGATAAATGGGATCAGGTGCCGTGATGCTGAGAACTGCTGT
GGCATCTCCAAGACAGAGGAAAGGGAGATCCAGTGCAGTGGCTACACGCTACCCACCAAGGTGGCCAAGGAGTGC
AGCTGCCAGCGGTGTACGGAACCTCGGAGCATCGTGCGGGGCCGTGTGCTGCTGCTGACAAATGGGGAGCCCATG
CGCTTTGGCCATGTGTACATGGGGAACAGCCGTGTAAGCATGACTGGCTACAAGGGCACTTTCACCTCATGTC
CCCCAGGACACTGAGAGGCTGGTGTCTACATTTGTGGACAGGCTGCAGAAGTTTGTCAACACCACCAAAAGTGCTA
CCTTTCAACAAGAGGGGAGTGCCGTGTTCCATGAAATCAAGATGCTTCCGTGGAAAGAGCCCATCACTTTGGAA
GCCATGAGAGCAACATCATCCCCCTGGGGGAAGTGGTTGGTGAAGACCCCATGGCTGAAGTGGAGTTCCATCC
AGGAGTTTCTACAGGCAGAAATGGGGAGCCCTACATAGGAAAAGTGAAGGCCAGTGTGACCTTCTGGATCCCCGG
AATATTTCCACAGCCACAGCTGCCAGACTGACCTGAATTCATCAATGACGAAGGAGACACTTTCCCTTTCGG
ACGTATGGCCATGTTCTCTGTGGACTTCAGAGATGAGGTCACTGACAGCCACTTAATGCTGGCAAAGTGAAGTGC
CACCTTGACTCGACCCAGGTCAAGATGCCAGAGACATATCCACAGTGAAGTCTGGTCACTCAATCCAGACACA
GGGCTGTGGGAGGAGGAAGGTGATTTCAAATTTGAAAATCAAAGGAGGAACAAAAGAGAAGCAGAACTTCTCTG
GTGGGCAACCTGGAGATTCTGTGAGAGGAGGCTCTTAACTGGATGTTCTGAAAGCAGGCGGTGCTTGTAAAG
GTGAGGGCTACCCGAGTGAGAGGTTCTTGCCTAGTGAGCAGATCCAGGGGGTGTGATCTCCGTGATTAACTG
GAGCTAGAAGTGGCTTCTGTGTCACCCCTAGGGCTGGGGCCGCTTGTGACAGTGTCTACAGGGCCCAACGGG
GCCTGTGTGCTGCTTCTGTGATGACCACTGCCCTGATGCTACTCTGCTATGTCTTGGCAAGCCTGGCTGGG
GAGGAATGCAAGCAGTGGAGTCTTCTCTAAATTCACCCAAATGCAATTGGCGTCCCTCAGCCCTATCTCAAC
AAGCTCAACTACCGTCGGACGGACCATGAGGATCCACGGGTTAAAAAGACAGCTTTCCAGATTAGCATGGCCAAG
CCAAGGCCCAACTCAGCTGAGGAGAGCAATGGGCCATCTATGCCCTTGTGAGAACCTCCGGGCATGTGAAGAGGCA
CCACCCAGTCAGCCCACTTCCGGTCTTACCAGATTGAGGGGGATCGATATGACTACAACACAGTCCCCCTCAAC
GAAGATGACCTATGAGCTGGACTGAAGACTATCTGGCATGGTGGCCAAAGCCGATGGAATTCAGGGCCTGCTAT
ATCAAGGTGAAGATTGTGGGGCCACTGGAAGTGAATGTGCGATCCCGCAACATGGGGGGCACTCATCGGCGGACA
GTGGGGAAGCTGTATGGAATCCGAGATGTGAGGAGCACTCGGGACAGGGACCAGCCCAATGTCTCAGCTGCCTGT
CTGGAGTTCAAGTGCAGTGGGATGCTCTATGATCAGGACCGTGTGGACCGCACCTGGTGAAGGTCACTCCCCAG
GGCAGCTGCCGTGAGCCAGTGTGAACCCCATGCTGCATGAGTACCTGGTCAACCACTTGCCACTTGCAGTCAAC
AACGACACCAAGTGAAGTACACCATGCTGGCACCTTGGACCCACTGGGGCCCAACTATGGCATCTACACTGTCACT
GACCAGGACCTCGCACGGCCAAGGAGATCGCGCTCGGCCGGTGTGATGGCACATCCGATGGCTCCTCCAGA
ATCATGAAGAGCAATGTGGGAGTAGCCCTCACCTTCAACTGTGTAGAGAGGCAAGTAGGCCGCCAGAGTGCCTTC
CAGTACCTCCAAAGCACCCAGCCAGTCCCCTGCTGCAGGCACTGTCCAAGGAAGAGTGCCTCGAGGAGGCGAG
CAGCGAGCGAGCAGGGGTGGCCAGCGCCAGGGTGGAGTGGTGGCTCTCTGAGATTTCTAGAGTTGCTCAACAG
CCCCTGATCAACTAAAGTTTGTGGTACTTCACCTCTTCTGCCCTCATTTTCATGTGACAGCCATTGTGAGACTGA
TGCACAAACTGTCACTTGGTTAATTTAAGCACTTCTGTTTTCTGTAATTTGCTTGTGTTTTCTTTCATGCCCTTA
CTTACTTTGTCCCATGCTACTGATTGGCACGTGGCCCCCAATGGCACAAATAAAGCCCCTTGTGAAACTGTTT
TTTAAATGAAACACAAGAAATTTGGCCACTGGTAAACTCTGCAGCTTCAACTGTACTTCAATTAATGCCATTAAT
GCAATATACTTCTCTTCTTTTGTGATGGTTTTTGGCCACCTCTGCAATAGTGATAATCTGATGCTGAAGATCAA
ATAACCAATATAAAGCATATTTCTTGGCCTTGCTCCACAGGACATAGGCAAGCCTTGATCATAGTTTCATACATAT
AAATGGTGGTGAAATAAAGAAATAAAACACAATACTTTTACTTGAAATGTAAATAACTTATTTATTTCTTTGCTA
AATTTGGAATTTAGTGACATTCAAAGTTAAGCTATTAATATAGGGTGATCATAGTTTCTCTACCAAGTCTGG
AAAGAACATCTCCTGGTATCCACAATTACACCAGGTTGCTAACTGTATTGTACATTTCCCTTTGCATTGCTTT
TGTTCTTGCTAGAAACCCAGTGTAGCCAGGGCAGATGTCAATAAATGCATACTCTGTATTTGAAAAA

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FIGURE 412

MVGTKAWVFSFLVLEVTSVLGRQTMLTQSVRRVQPGKKNPSIFAKPADTLESPGEWTTWFNID
YPGGKGDYERLDAIRFYYGDRVCARPLRLEARTTDWTPAGSTGQVVHGSPREGFWCLNREQRP
GQNCSNYTVRFLCPPGSLRRDTERIWS PWSPWSKCSAACGQTGVQTRTRICLAEMVSLCSEAS
EEGQHCMGQDCTACDLTC PMGQVNADCDACMCQDFMLHGAVSLPGGAPASGAAYLLTKTPKL
LTQTDS DGRFRIPGLCPDGKSILKITKVKFAPIVLTMPKTS LKAATIKAEFVRAETPYMVMNP
ETKARRAGQSVSLCCKATGKPRPDKYFWYHNDTLLDPSLYKHESKLVLRLKLOQH QAGEYFCKA
QSDAGAVKSKVAQLIVTASDETPCNPVPESYLIRLPHDCFQ NATNSFYVDVGRCPVKTCAGQQ
DNGIRCRDAVQNC CGISKTEEREIQCSGYTLPTKVAKECSCQRCTETRSIVRGRVSAADNGEP
MRFGHVYMGNSRVSM TGYKGTFTLHVPQDTERLVLT FVDRLQKFVN TTKVL PFKKGS AVFHE
IKMLRRKEPIT LEAMETNII PLGEVVGEDPMAELEIPSR SFYRQNGEPYIGKVKASVTFLDPR
NISTATAAQTD LNF INDEGDTFPLRTYGMFSVDFRDEVTSEPLNAGKVKVHLDSTQVKMPEHI
STVKLWSLNPDTGLWEEEGDFKFENQRRNKREDRTFLVGNLEIRERRLFNLDPESRRCFVKV
RAYRSE RFLPSEQIQGVVISVINLEPRTGFLSNPRAWGRFDSVITGPNGACVPAFCDDQSPDA
YSAYVLASLAGEELQAVESSPKFNPNAIGVPQPYLNKLNRYRRTDHEDPRVKKTAFQISMAKPR
PNSAEESNGPIYAFENLRACEEAPPSAAHFRFYQIEGDRYDYNTVPFNEDDPMSWTEDYLAWW
PKPMEFRACYIKVKIVGPLEVNVR SRNMGGTHRRTVGKLYGIRDVRSTRDRDQPNVSAACLEF
KCSGMLYDQDRVDRTL VKVIPQGSCRRASVN PMLHEYLVNHLPLAVNNDTSEYTMLAPLDPLG
HNYGIYTVTDQDPRTAKEIALGRCFDGTS DGSSRIMKSNVGVALT FNCVERQVGRQSAFQYLQ
STPAQSPAAGTVQGRVPSRRQQRASRGGQRQGGVVASLRFPRVAQQPLIN

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FIGURE 413

GCCACGTTGTCTTCTTTCTTCACCACCACCCAGGAGCTCAGAGATCTAAGCTGCTTTCCATC
TTTTCTCCCAGCCCCAGGACACTGACTCTGTACAGGATGGGGCCGTCCTCTTGCCCTCCTTCTC
ATCCTAATCCCCCTTCTCCAGCTGATCAACCCGGGGAGTACTCAGTGTTCTTAGACTCCGTT
ATGGATAAGAAGATCAAGGATGTTCTCAACAGTCTAGAGTACAGTCCCTCTCCTATAAGCAAG
AAGCTCTCGTGTGCTAGTGTCAAAAGCCAAGGCAGACCGTCCTCCTGCCCTGCTGGGATGGCT
GTCACTGGCTGTGCTTGTGGCTATGGCTGTGGTTCGTGGGATGTTTCAGCTGGAAACCACCTGC
CACTGCCAGTGCAGTGTGGTGGACTGGACCACTGCCCGCTGCTGCCACCTGACCTTGACAGGGA
GGAGGCTGAGAACTCAGTTTTGTGACCATGACAGTAATGAAACCAGGGTCCCAACCAAGAAAT
CTAACTCAAACGTCCCACCTTCATTTGTTCCATTCCTGATTCTTGGGTAATAAAGACAAACTTT
GTACCTCAAAAAAAAAAAAAAAAAAAAAA

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FIGURE 414

MGPSSCLLLILIPLLQLINPGSTQCSLDSVMDKKIKDVLNSLEYSPSPISKKLSCASVKS
QGRPSSCPAGMAVTGCACGYGCGSWDVQLETTCHCQCSVVDWTTARCCHLT

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FIGURE 415

CAGAAGAGGGGGCTAGCTAGCTGTCTCTGCGGACCAGGGAGACCCCCGCGCCCCCCCCGGTGTG
AGGCGGCCTCACAGGGCCGGGTGGGCTGGCGAGCCGACGCGGCGGCGGAGGAGGCTGTGAGGA
GTGTGTGGAACAGGACCCGGGACAGAGGAACCATGGCTCCGCAGAACCTGAGCACCTTTTGCC
TGTTGCTGCTATACCTCATCGGGGCGGTGATTGCCGGACGAGATTTCTATAAGATCTTGGGGG
TGCCTCGAAGTGCCTCTATAAAGGATATTAAGGCTATAGGAACTAGCCCTGCAGCTTC
ATCCCGACCGGAACCCTGATGATCCACAAGCCCAGGAGAAATTCAGGATCTGGGTGCTGCTT
ATGAGGTTCTGTGAGATAGTGAGAAACGGAAACAGTACGATACTTATGGTGAAGAAGGATTAA
AAGATGGTCATCAGAGCTCCCATGGAGACATTTTTTTCACACTTCTTTGGGGATTTTGGTTTCA
TGTTTGGAGGAACCCCTCGTCAGCAAGACAGAAATATTCGAAGAGGAAGTGATATTATTGTAG
ATCTAGAAGTCACTTTGGAAGAAGTATATGCAGGAAATTTTGTGGAAGTAGTTAGAAACAAAC
CTGTGGCAAGGCAGGCTCCTGGCAAACGGAAGTGCAATTGTCGGCAAGAGATGCGGACCACCC
AGCTGGGCCCTGGGCGCTTCCAAATGACCCAGGAGGTGGTCTGCGACGAATGCCCTAATGTCA
AACTAGTGAATGAAGAACGAACGCTGGAAGTAGAAATAGAGCCTGGGGTGAGAGACGGCATGG
AGTACCCCTTTATTGGAGAAGGTGAGCCTCACGTGGATGGGGAGCCTGGAGATTTACGGTTCC
GAATCAAAGTTGTCAAGCACCCAATATTTGAAAGGAGAGGAGATGATTTGTACACAAATGTGA
CAATCTCATTAGTTGAGTCACTGGTTGGCTTTGAGATGGATATTACTCACTTGGATGGTCACA
AGGTACATATTTCCCGGGATAAGATCACCAGGCCAGGAGCGAAGCTATGGAAGAAAGGGGAAG
GGCTCCCCAACTTTGACAACAACAATATCAAGGGCTCTTTGATAATCACTTTTGATGTGGATT
TTCCAAAAGAACAGTTAACAGAGGAAGCGAGAGAAGGTATCAAACAGCTACTGAAACAAGGGT
CAGTGCAGAAGGTATACAATGGACTGCAAGGATATTGAGAGTGAATAAAATTGGACTTTGTTT
AAAATAAGTGAATAAGCGATATTTATTATCTGCAAGGTTTTTTTTGTGTGTGTTTTTGTTTTTA
TTTTCAATATGCAAGTTAGGCTTAATTTTTTTTATCTAATGATCATCATGAAATGAATAAGAGG
GCTTAAGAATTTGTCCATTTGCATTCGGAAAAGAATGACCAGCAAAGGTTTACTAATACCTC
TCCCTTTGGGGATTTAATGTCTGGTGCTGCCGCCTGAGTTTCAAGAATTAAAGCTGCAAGAGG
ACTCCAGGAGCAAAGAAACACAATATAGAGGGTTGGAGTTGTTAGCAATTTCAATTCAAAATG
CCAATGGAGAAGTCTGTTTTTAAATACATTTTGTTGTTATTTTTA

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FIGURE 416

MAPQNLSTFCLLLLYLIGAVIAGRDFYKILGVPRSASIKDIKKAYRKALQLHPDRNPDDPQAQEKFDLGAAYE
VLSDSEKRKQYDITYGEEGLKDGHQSSHGDIFSHFFGDFGFMFGGTPRQQDRNIPRGSDIIVDLEVTL EEVYAGNF
VEVVRNKPVARQAPGKRKCNCRQEMRTTQLGPGRFQMTQEVVCDECPNVKLVNEERTLEVEIEPGVRDGMEYPFI
GEGEPHVDGEPGDLRFRIKVVKHPIFERRGDDLYTNVTISLVESLVGFEMDITHLDGHKVVHISRDKITRPGAKLW
KKGEGLPNFDNNNIKGLIITFDVDFPKEQLTEEAREGIKQLLKQGSVQKVYNGLQGY

Important features:**Signal peptide:**

amino acids 1-22

Cell attachment sequence.

amino acids 254-257

Nt-dnaJ domain signature.

amino acids 67-87

Homologous region to Nt-dnaJ domain proteins.

amino acids 26-58

N-glycosylation site.

amino acids 5-9, 261-265

Tyrosine kinase phosphorylation site.

amino acids 253-260

N-myristoylation site.

amino acids 18-24, 31-37, 93-99, 215-221

Amidation site.

amino acids 164-168

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FIGURE 417

CGGCGGCGGCTGCGGGCGCGAGGTGAGGGGCGCGAGGTGAGGGGCGCGAGGTTCCCAGCAGGA
TGCCCCGGCTCTGCAGGAAGCTGAAGTGAGAGGCCCGGAGAGGGCCCAGCCCGCCGGGGCAG
GATGACCAAGGCCCGGCTGTTCCGGCTGTGGCTGGTGCTGGGGTCGGTGTTTCATGATCCTGCT
GATCATCGTGTA TACTGGGACAGCGCAGGCGCCGCGCACTTCTACTTGACACAGTCCTTCTCTAG
GCCGCACACGGGGCCGCGCTGCCACGCCCCGGGCGGACAGGGACAGGGAGCTCACGGCCGA
CTCCGATGTCGACGAGTTTCTGGACAAGTTTCTCAGTGCTGGCGTGAAGCAGAGCGACCTTCC
CAGAAAGGAGACGGAGCAGCCGCTGCGCCGGGGAGCATGGAGGAGAGCGTGAGAGGCTACGA
CTGGTCCCCGCGCGACGCCCGGCGCAGCCAGACCAGGGCCGGCAGCAGGCGGAGCGGAGGAG
CGTGCTGCGGGGCTTCTGCGCCAACTCCAGCCTGGCCTTCCCCACCAAGGAGCGCGCATTTCGA
CGACATCCCCAACTCGGAGCTGAGCCACCTGATCGTGACGACCGGCACGGGGCCATCTACTG
CTACGTGCCCCAAGGTGGCCTGCACCAACTGGAAGCGCGTGATGATCGTGCTGAGCGGAAGCCT
GCTGCACCGCGGTGCGCCCTACCGCGACCCGCTGCGCATCCCGCGCGAGCACGTGCACAACGC
CAGCGCGCACCTGACCTTCAACAAGTTCTGGCGCCGCTACGGGAAGCTCTCCCGCCACCTCAT
GAAGGTCAAGCTCAAGAAGTACACCAAGTTCTTCTTCGTGCGCGACCCCTTCGTGCGCCTGAT
CTCCGCCTTCCGCAGCAAGTTCGAGCTGGAGAACGAGGAGTTCTACCGCAAGTTCGCCGTGCC
CATGCTGCGGCTGTACGCCAACCACACCAGCCTGCCCCGCTCGGCGCGCGAGGCCTTCCGCGC
TGGCCTCAAGGTGTCCTTCGCCAACTTCATCCAGTACCTGCTGGACCCGCACACGGAGAAGCT
GGCGCCCTTCAACGAGCACTGGCGGCAGGTGTACCGCCTCTGCCACCCGTGCCAGATCGACTA
CGACTTCGTGGGGAAGCTGGAGACTCTGGACGAGGACGCCGCGCAGCTGCTGCAGCTACTCCA
GGTGGACCGGCAGCTCCGCTTCCCCCGAGCTACCGGAACAGGACCGCCAGCAGCTGGGAGGA
GGACTGGTTCGCCAAGATCCCCTGGCCTGGAGGCAGCAGCTGTATAAACTCTACGAGGCCGA
CTTTGTTCTCTTCGGCTACCCCAAGCCCGAAAACCTCCTCCGAGACTGAAAGCTTTCGCGTTG
CTTTTTCTCGCGTGCTGGAACCTGACGCACGCGCACTCCAGTTTTTTTTATGACCTACGATTT
TGCAATCTGGGCTTCTTGTTCACTCCACTGCCTCTATCCATTGAGTACTGTATCGATATTGTT
TTTTAAGATTAATATATTTTCAGGTATTTAATACGA

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FIGURE 418

MTKARLFRLWLVLGSVFMILLIIIVYWDSAGAAHFYLHTSF SRPHTGPPLPTPGPDRDRELTAD
SDVDEFLDKFLSAGVKQSDLPRKETEQPPAPGSMEE SVRGYDWSPRDARRSPDQGRQQAERRS
VLRGFCANSSLAFPTKERAFFDDIPNSEL SHLIVDDRHGAIYCYVPKVACTNWK RVMIVLSGSL
LHRGAPYRDPLRIPREHVHNASAHLT FNKFWRRYGKLSRHLMKVKLKKYTKFLFVRDPFVRLI
SAFRSKFELENEEFYRKFAVPMLRLYANHTSLPASAREAFRAGLKVSFANFIQYLLDPHTEKL
APFNEHWRQVYRLCHPCQIDYDFVGKLETLD EDAAQLLQLLQVDRQLRFPPSYRNR TASSWEE
DWFAKIPLAWRQQLYKLYEADFVLF GYPKPENLLRD

Important features:**Signal peptide:**

amino acids 1-31

N-glycosylation sites.

amino acids 134-137, 209-212, 280-283 and 370-373

TNFR/NGFR family cysteine-rich region protein

amino acids 329-332

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FIGURE 419

GGCACGAGGCTGAACCCAGCCGGCTCCATCTCAGCTTCTGGTTTCTAAGTCCATGTGCCAAAG
GCTGCCAGGAAGGAGACGCCTTCCTGAGTCCTGGATCTTTCTTCCTTCTGGAAATCTTTGACT
GTGGGTAGTTATTTATTTCTGAATAAGAGCGTCCACGCATCATGGACCTCGCGGGACTGCTGA
AGTCTCAGTTCCTGTGCCACCTGGTCTTCTGCTACGTCTTTATTGCCTCAGGGCTAATCATCA
ACACCATTTCAGCTCTTCACTCTCCTCCTCTGGCCCATTAACAAGCAGCTCTTCCGGAAGATCA
ACTGCAGACTGTCCTATTGCATCTCAAGCCAGCTGGTGATGCTGCTGGAGTGGTGGTCGGGCA
CGGAATGCACCATCTTCACGGACCCGCGCGCCTACCTCAAGTATGGGAAGGAAAATGCCATCG
TGTTTCTCAACCACAAGTTTGAAATTGACTTTCTGTGTGGCTGGAGCCTGTCCGAACGCTTTG
GGCTGTTAGGGGGCTCCAAGGTCTTGCCCAAGAAAGAGCTGGCCTATGTCCCAATTATCGGCT
GGATGTGGTACTTCACCGAGATGGTCTTCTGTTCGCGCAAGTGGGAGCAGGATCGCAAGACGG
TTGCCACCAGTTTGCAGCACCTCCGGGACTACCCCGAGAAGTATTTTTTCTGATTCACTGTG
AGGGCACACGGTTCACGGAGAAGAAGCATGAGATCAGCATGCAGGTGGCCCGGGCCAAGGGGC
TGCCTCGCCTCAAGCATCACCTGTTGCCACGAACCAAGGGCTTCGCCATCACCGTGAGGAGCT
TGAGAAATGTAGTTTCAGCTGTATATGACTGTACACTCAATTCAGAAATAATGAAAATCCAA
CACTGCTGGGAGTCCTAAACGGAAAGAAATACCATGCAGATTTGTATGTTAGGAGGATCCCAC
TGGAAGACATCCCTGAAGACGATGACGAGTGCTCGGCCTGGCTGCACAAGCTCTACCAGGAGA
AGGATGCCTTTTCAGGAGGAGTACTACAGGACGGGCACCTTCCCAGAGACGCCCATGGTGCCCC
CCCGGCGGCCCTGGACCCTCGTGAACCTGGCTGTTTTGGGCCTCGCTGGTGCTCTACCCTTTCT
TCCAGTTCTTGGTTCAGCATGATCAGGAGCGGGTCTTCCCTGACGCTGGCCAGCTTCATCCTCG
TCTTCTTTGTGGCCTCCGTGGGAGTTCGATGGATGATTGGTGTGACGGAAATTGACAAGGGCT
CTGCCTACGGCAACTCTGACAGCAAGCAGAACTGAATGACTGACTCAGGGAGGTGTCACCAT
CCGAAGGGAACCTTGGGGAACCTGGTGGCCTCTGCATATCCTCCTTAGTGGGACACGGTGACAA
AGGCTGGGTGAGCCCCCTGCTGGGCACGGCGGAAGTCACGACCTCTCCAGCCAGGGAGTCTGGT
CTCAAGGCCGGATGGGGAGGAAGATGTTTTGTAATCTTTTTTTCCCATGTGCTTTAGTGGGC
TTTGGTTTTCTTTTTGTGCGAGTGTGTGTGAGAATGGCTGTGTGGTGAGTGTGAACTTTGTTC
TGTGATCATAGAAAGGGTATTTTAGGCTGCAGGGGAGGGCAGGGCTGGGGACCGAAGGGGACA
AGTTCCTCTTTCATCCTTTGGTGCTGAGTTTTCTGTAACCCTTGGTTGCCAGAGATAAAGTGA
AAAGTGCTTTAGGTGAGATGACTAAATTATGCCTCCAAGAAAAAAAATTAAGTGCTTTTCT
GGGTCAAAAAAAAAAAAA

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FIGURE 420

MDLAGLLKSQFLCHLVFCYVFIA SGLIINTIQLFTLLLWPINKQLFRKINCRLSYCISSQLVM
LLEWWSGTECTIFTDPRAYLKYGKENAIVVLNHNHFEIDFLCGWSLSERFGLLGGSKVLAKKEL
AYVPIIGWMWYFTEMVFCSRKWEQDRKTVATSLQHLDYPEKYFFLIHCEGTRFTEKKHEISM
QVARAKGLPRLKHHLLPRTKGFAITVRSLRNVVSAVYDCTLNFRNNENPTLLGVLNGKKYHAD
LYVRRIPLEDIPEDDDECSAWLHKLYQEKDAFQEEYYRTGTFPETPMVPPRRPWTLVNWLFWA
SLVLYPFFQFLVSMIRSGSSLTLASFILVFFVASVGVRWMIGVTEIDKGSAYGNSDSKQKLND

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FIGURE 421

CGGACGCGTGGGCGGACGCGTGGGCGGACGCGTGGGCGGACGCGTGGGCTGGGTGCCTGCATC
GCC**ATG**GACACCACCAGGTACAGCAAGTGGGGCGGCAGCTCCGAGGAGGTCCCCGGAGGGCCC
TGGGGACGCTGGGTGCACTGGAGCAGGAGACCCCTCTTCTTGGCCCTGGCTGTCCTGGTCACC
ACAGTCCTTTGGGCTGTGATTCTGAGTATCCTATTGTCCAAGGCCTCCACGGAGCGCGCGGCG
CTGCTTGACGGCCACGACCTGCTGAGGACAAACGCCTCGAAGCAGACGGCGGGCGCTGGGTGCC
CTGAAGGAGGAGGTCTGGAGACTGCCACAGCTGCTGCTCGGGGACGCAGGCGCAGCTGCAGACC
ACGCGCGCGGAGCTTGGGGAGGCGCAGGCGAAGCTGATGGAGCAGGAGAGCGCCCTGCGGGAA
CTGCGTGAGCGCGTGACCCAGGGCTTGGCTGAAGCCGGCAGGGGCCGTGAGGACGTCCGCACT
GAGCTGTTCCGGGCGCTGGAGGCCGTGAGGCTCCAGAACAACCTCTGCGAGCCGTGCCCCACG
TCGTGGCTGTCCTTCGAGGGCTCCTGCTACTTTTTCTCTGTGCCAAAGACGACGTGGGCGGCG
GCGCAGGATCACTGCGCAGATGCCAGCGCGCACCTGGTGATCGTTGGGGGCCTGGATGAGCAG
GGCTTCCTCACTCGGAACACGCGTGGCCGTGGTTACTGGCTGGGCCTGAGGGCTGTGCGCCAT
CTGGGCAAGGTTTCAAGGGCTACCAAGTGGGTGGACGGAGTCTCTCTCAGCTTCAGCCACTGGAAC
CAGGGAGAGCCCAATGACGCTTGGGGGCGCGAGAACTGTGTCATGATGCTGCACACGGGGCTG
TGGAACGACGCACCGTGTGACAGCGAGAAGGACGGCTGGATCTGTGAGAAAAGGCACAACCTGC
TGACCCCGCCCAGTGCCCTGGAGCCGCGCCCATTTGCAGCATGTCGTATCCTGGGGGCTGCTCA
CCTCCCTGGCTCCTGGAGCTGATTGCCAAAGAGTTTTTTTTCTTCTCATCCACCGCTGCTGAG
TCTCAGAAACACTTGGCCCAACATAGCCCTGTCCAGCCCAGTGCCTGGGCTCTGGGACCTCCA
TGCCGACCTCATCCTAACTCCACTCACGCAGACCCAACCTAACCTCCACTAGCTCCAAAATCC
CTGCTCCTGCGTCCCCGTGATATGCCTCCACTTCTCTCCCTAACCAAGGTTAGGTGACTGAGG
ACTGGAGCTGTTTTGGTTTTTCTCGCATTTTCCACCAAACCTGGAAGCTGTTTTTGCAGCCTGAGG
AAGCATCAATAAATATTTGAGAAATGAAAAA

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FIGURE 422

MDTTRYSKWGSSEEVPGGPWGRVHWSRRPLFLALAVLVTTVLWAVILSILLSKASTERAAL
LDGHDLLRTNASKQTAALGALKEEVGDCHSCCSGTQAQLQTTRAEELGEAQAKLMEQESALREL
RERVTQGLAEAGRGREDVRTELFRALAVRLQNNSCPCPTSWLSFEGSCYFFSVPKTTWAAA
QDHCADASAHLVIVGGLDEQGFLTRNTRGRGYWLGLRAVRHLGKVQGYQWVDGVSLSFHWNQ
GEPNDAWGRENVMMLHTGLWNDAPCDSEKDGWICEKRHNC

Important features:**Type II transmembrane domain:**

amino acids 31-54

N-glycosylation sites.

amino acids 73-76 and 159-162

Leucine zipper pattern.

amino acids 102-123

N-myristoylation sites.

amino acids 18-23, 133-138 and 242-247

C-type lectin domain signature.

amino acids 264-287

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FIGURE 423

GCGCCGCCAGGCGTAGGCGGGGTGGCCCTTGCGTCTCCCGCTTCCTTGAAAAACCCGGCGGGC
GAGCGAGGCTGCGGGCCGGCCGCTGCCCTTCCCCACACTCCCCGCCGAGAAGCCTCGCTCGGC
GCCCAAC**ATGG**CGGGTGGGCGCTGCGGCCCCGAGCTAACGGCGCTCCTGGCCGCCTGGATCGC
GGCTGTGGCGGCGACGGCAGGCCCCGAGGAGGCCGCGCTGCCGCCGAGCAGAGCCGGGTCCA
GCCCATGACCGCCTCCAACTGGACGCTGGTGATGGAGGGCGAGTGGATGCTGAAATTTTACGC
CCCATGGTGTCCATCCTGCCAGCAGACTGATTCAGAATGGGAGGCTTTTGCAAAGAATGGTGA
AATACTTCAGATCAGTGTGGGGAAGGTAGATGTCATTCAAGAACCAGGTTTGAGTGGCCGCTT
CTTTGTCACCACTCTCCCAGCATTTTTTTCATGCAAAGGATGGGATATTCCGCCGTTATCGTGG
CCCAGGAATCTTCGAAGACCTGCAGAATTATATCTTAGAGAAGAAATGGCAATCAGTCGAGCC
TCTGACTGGCTGGAAATCCCCAGCTTCTCTAACGATGTCTGGAATGGCTGGTCTTTTTAGCAT
CTCTGGCAAGATATGGCATCTTCACAACATTTTCACAGTGAAGTCTTGGAAATCCTGCTTGGTG
TTCTTATGTGTTTTTTCGTATAGCCACCTTGGTTTTTGGCCTTTTTATGGGTCTGGTCTTGGT
GGTAATATCAGAATGTTTCTATGTGCCACTTCCAAGGCATTTATCTGAGCGTTCTGAGCAGAA
TCGGAGATCAGAGGAGGCTCATAGAGCTGAACAGTTGCAGGATGCGGAGGAGGAAAAAGATGA
TTCAAATGAAGAAGAAAACAAAGACAGCCTTGTAAGATGATGAAGAAGAGAAAGAAGATCTTGG
CGATGAGGATGAAGCAGAGGAAGAAGAGGAGGAGGACAACTTGGCTGCTGGTGTGGATGAGGA
GAGAAGTGAGGCCAATGATCAGGGGCCCCCAGGAGAGGACGGTGTGACCCGGGAGGAAGTAGA
GCCTGAGGAGGCTGAAGAAGGCATCTCTGAGCAACCTTGCCCAGCTGACACAGAGGTGGTGGGA
AGACTCCTTGAGGCAGCGTAAAAGTCAGCATGCTGACAAGGGACTG**TAG**ATTTAATGATGCGT
TTTCAAGAATACACACCAAAACAATATGTCAGCTTCCCTTTGGCCTGCAGTTTGTACCAAATC
CTTAATTTTTTCTGAATGAGCAAGCTTCTCTTAAAGATGCTCTCTAGTCATTTGGTCTCATG
GCAGTAAGCCTCATGTATACTAAGGAGAGTCTTCCAGGTGTGACAATCAGGATATAGAAAAAC
AAACGTAGTGTTGGGATCTGTTTGGAGACTGGGATGGGAACAAGTTCATTTACTTAGGGGTCA
GAGAGTCTCGACCAGAGGAGGCCATTCCCAGTCCTAATCAGCACCTTCCAGAGACAAGGCTGC
AGGCCCTGTGAAATGAAAGCCAAGCAGGAGCCTTGGCTCCTGAGCATCCCCAAAGTGTAACGT
AGAAGCCTTGCATCCTTTTTCTTGTGTAAAGTATTTATTTTTGTCAAATTGCAGGAAACATCAG
GCACCACAGTGCATGAAAAATCTTTCACAGCTAGAAATTGAAAGGGCCTTGGGTATAGAGAGC
AGCTCAGAAGTCATCCCAGCCCTCTGAATCTCCTGTGCTATGTTTTATTTCTTACCTTTAATT
TTTCCAGCATTTCCACCATGGGCATTACAGGCTCTCCACACTCTTCACTATTATCTCTTGGTCA
GAGGACTCCAATAACAGCCAGGTTTACATGAACTGTGTTTGTTCATTCTGACCTAAGGGGTTT
AGATAATCAGTAACCATAACCCCTGAAGCTGTGACTGCCAAACATCTCAAATGAAATGTTGTG
GCCATCAGAGACTCAAAAGGAAGTAAGGATTTTACAAGACAGATTAAAAAAAATTGTTTTGT
CCAAAATATAGTTGTTGTTGATTTTTTTTTTAAGTTTTCTAAGCAATATTTTTCAAGCCAGAAG
TCCTCTAAGTCTTGCCAGTACAAGGTAGTCTTGTGAAGAAAAGTTGAATACTGTTTTGTTTTT
ATCTCAAGGGGTTCCCTGGGTCTTGAAGTACTTTAATAATAACTAAAAAACCACTTCTGATTT
TCCTTCAGTGATGTGCTTTTGGTGAAAGAATTAATGAAGTCCAGTACCTGAAAGTGAAAGATT
TGATTTTGTTCATCTTCTGTAATCTTCCAAAGAATTATATCTTTGTAAATCTCTCAATACT
CAATCTACTGTAAGTACCCAGGGAGGCTAATTTCTTT

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FIGURE 424

MAGGRCGPQLTALLAAWIAAVAATAGPEEAALPPEQSRVQPMTASNWTLVMEGEWMLKFYAPW
CPSCQQTDSEWEAFKNGEILQISVGKVDVIQEPGLSGRFFVTTLPAFFHAKDGI FRRYRGPG
IFEDLQNYILEKKWQSVEPLTGWKSPASLTMSGMAGLFSISGKIWHLHNYFTVTLGIPAWCSY
VFFVIATLVFGLFMGLVLVVISSECFYVPLPRHLSESEQNRRSEEAHRAEQLQDAEEEKDDSN
EENKDSLVDDEEEKEDLGDEDEAEEDNLAAGVDEERSEANDQGPPGEDGVTREEVEPE
EAEEGISEQPCPADTEVVEDSLRQRKSQHADKGL

Important features:**Signal peptide:**

amino acids 1-22

Transmembrane domain:

amino acids 191-211

N-glycosylation site.

amino acids 46-49

Thioredoxin family proteins. (homologous region to disulfide
isomerase)

amino acids 56-72

Flavodoxin proteins

amino acids 173-187

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FIGURE 425

GAGGAACCTACCGGTACCGGCCGCGCGCTGGTAGTCGCCGGTGTGGCTGCACCTCACCAATCCCGTGCGCCGCGG
CTGGGCCGTCGGAGAGTGCCTGTGCTTCTCTCCTGCACGCGGTGCTTGGGCTCGGCCAGGCGGGGTCCGCCGCCA
GGGTTTGAGGATGGGGGAGTAGCTACAGGAAGCGACCCCGCGATGGCAAGGTATATTTTTGTGGAATGAAAAGGA
AGTATTAGAAATGAGCTGAAGACCATTACAGATTAATATTTTTGGGGACAGATTTGTGATGCTTGATTCACCCT
TGAAGTAATGTAGACAGAAGTTCTCAAATTTGCATATTACATCAACTGGAACCAGCAGTGAATCTTAATGTTTAC
TTAAATCAGAACTTGCATAAGAAAGAGAAATGGGAGTCTGGTTAAATAAAGATGACTATATCAGAGACTTGAAAAG
GATCATTCTCTGTTTTCTGATAGTGTATATGGCCATTTTAGTGGGCACAGATCAGGATTTTTACAGTTTACTTGG
AGTGTCCAAAACCTGCAAGCAGTAGAGAAATAAGACAAGCTTCAAGAAATTGGCATTGAAGTTACATCCTGATAA
AAACCCGAATAACCCAAATGCACATGGCGATTTTTTAAAAATAAATAGAGCATATGAAGTACTCAAAGATGAAGA
TCTACGGAAAAAGTATGACAAATATGGAGAAAAGGGACTTGAGGATAATCAAGGTGGCCAGTATGAAAGCTGGAA
CTATTATCGTTATGATTTTTGGTATTTATGATGATGATCCTGAAATCATAACATTGGAAAGAAGAGAATTTGATGC
TGCTGTTAATTCTGGAGAACTGTGGTTTTGTAAATTTTTACTCCCCAGGCTGTTTCACTGCCATGATTTAGCTCC
CACATGGAGAGACTTTGCTAAAGAAGTGGATGGGTACTTCGAATTGGAGCTGTTAACTGTGGTGTATGATAGAAT
GCTTTGCCGAATGAAAGGAGTCAACAGCTATCCAGCTCTCTCATTTTTTCGGTCTGGAATGGCCCCAGTGAATA
TCATGGAGACAGATCAAAGGAGAGTTTTAGTGAGTTTTGCAATGCAGCATGTTAGAAGTACAGTGACAGAACTTTG
GACAGGAAATTTTGTCAACTCCATACAACTGCTTTTGCTGCTGGTATTGGCTGGCTGATCACTTTTTGTTCAAA
AGGAGGAGATTGTTTGACTTCACAGACACGACTCAGGCTTAGTGGCATGTTGTTTTCTCAACTCATTGGATGCTAA
AGAAATATATTTGGAAGTAATACATAATCTTCCAGATTTTGAAGTACTTTCCGGCAAACACACTAGAGGATCGTTT
GGCTCATCATCGGTGGCTGTTATTTTTTCATTTTGGAAAAATGAAATTCAAATGATCCTGAGCTGAAAAAAT
AAAACTCTACTTAAAAATGATCATATTTCAAGTTGGCAGGTTTGACTGTTCCCTCTGCACCAGACATCTGTAGTAA
TCTGTATGTTTTTTCAGCCGTCTCTAGCAGTATTTAAAGGACAAGGAACCAAAGAATATGAAATTCATCATGGAAA
GAAGATTCTATATGATATACTTGCCTTTGCCAAAGAAAGTGTGAATTTCTCATGTTACCACGCTTGACCTCAAAA
TTTTCTGCCAATGACAAAGAACCATGGCTTGTGATTTCTTTGCCCCCTGGTGTCCACCATGTGCGAGCTTTACT
ACCAGAGTTACGAAGAGCATCAAATCTTCTTTATGGTCAGCTTAAGTTTGGTACACTAGATTGTACAGTTTCATGA
GGGACTCTGTAACATGTATAACATTCAGGCTTATCCAACAACAGTGGTATTCAACCAGTCCAACATTCATGAGTA
TGAAGGACATCACTCGCTGAACAAATCTTGAGGTTTCATAGAGGATCTTATGAATCCTTCAGTGGTCTCCCTTAC
ACCCACCACCTTCAACGAAGTATGTTACACAAAGAAAACACAACGAAGTCTGGATGGTTGATTTCTATTCTCCGTG
GTGTCATCCTTGCCAAGTCTTAATGCCAGAATGGAAGAAGTGGCCCGGACATTAAGTGGACTGATCAACGTGGG
CAGTATAGATTGCCAACAGTATCATTCTTTTTGTGCCAGGAAAACGTTCAAAGATACCCTGAGATAAGATTTTT
TCCCCCAAATCAAATAAGCTTATCAGTATCACAGTTACAATGGTTGGAATAGGGATGCTTATTCCTTGAGAAT
CTGGGGTCTAGGATTTTTACCTCAAGTATCCACAGATCAACACCTCAGACTTTCAGTGAAGAAAGTTCTACAAGG
GAAAAATCATTGGGTGATTGATTTCTATGCTCCTTGGTGTGGACCTTGCCAGAATTTTGCTCCAGAATTTGAGCT
CTTGGCTAGGATGATTAAAGGAAAAGTGAAGCTGGAAAAGTAGACTGTCAGGCTTATGCTCAGACATGCCAGAA
AGCTGGGATCAGGGCCTATCCAAGTGAAGTTTTATTTCTACGAAAGAGCAAAGAGAAATTTTCAAGAAGAGCA
GATAAATACCAGAGATGCAAAAGCAATCGCTGCCTTAATAAGTGAAGAAATTTGGAACTCTCCGAAATCAAGGCAA
GAGGAATAAGGATGAAGTTTGAATAATGTTGAAGATGAAGAAAAAGTTTAAAGAAATTTCTGACAGATGACATCAG
AAGACACCTATTTAGAATGTTACATTTATGATGGGAATGAATGAACATTATCTTAGACTTGCAGTTGTACTGCCA
GAATTTATCTACAGCACTGGTGTAAAAGAAGGGTCTGCAAACTTTTTCTGTAAAGGGCCGGTTTATAAATATTTTA
GACTTTGCAGGCTATAATATATGTTTACACATGAGAACAAGAATAGAGTCATCATGTATTCTTTGTTATTTGCT
TTTAAACACCTTTAAAAAATATTAAACGATTCTTAGCTCAGAGCCATACAAAAGTAGGCTGGATTAGTCCATG
GACCATAGATTGCTGTCCCCCTCGACGGACTTATAATGTTTCAAGTGGCTGGCTTGAACATGAGTCTGCTGTGCT
ATCTACATAAATGTCTAAGTTGTATAAAGTCCACTTTCCCTTCACGTTTTTTGGCTGACCTGAAAAGAGGTAAC
TAGTTTTTTGGTCACTTGTCTCCTAAAAATGCTATCCCTAACCATATATTTATATTTTCGTTTTAAAAACACCCAT
GATGTGGCACAGTAAACAAACCTGTTATGCTGTATTATTATGAGGAGATTCTTCATTGTTTTCTTTCTTCTCA
AAGGTTGAAAAATGCTTTTAATTTTTACAGCCGAGAAACAGTGCAGCAGTATATGTGCACACAGTAAGTACAC
AAATTTGAGCAACAGTAAGTGCACAAATCTGTAGTTTGTGTATCATCCAGGAAAACCTGAGGGAAAAAATTA
TAGCAATTAAGTGGGCATTGTAGAGTATCCTAAATATGTTATCAAGTATTTAGAGTTCTATATTTTAAAGATATA
TGTGTTTCATGTATTTCTGAAATGCTTTTCATAGAAATTTTCCCACTGATAGTTGATTTTTGAGGCATCTAATAT
TTACATATTTGCCTTCTGAACCTTTGTTTTGACCTGTATCCTTTATTTACATTGGGTTTTCTTTTATAGTTTGG
TTTTTCACTCCTGTCCAGTCTATTTATTATTTCAATAGGAAAAATTTTACAGGTTGTTTTACTGTAGCTTAT
AATGATACTGTAGTTATTTCCAGTTACTAGTTTACTGTGCAGAGGGCTGCCTTTTTTTCAGATAAATATTGACATAA
ACTGAAGTTATTTTTATAAGAAATCAAGTATATAAATCTAGGAAAGGGATCTTCTAGTTTCTGTGTTGTTTAGA
CTCAAAGAATCACAAATTTGTGAGTAACATGTAGTTGTTTAGTTATAATTTCAGAGTGTACAGAATGGTAAAAAT
CCAATCAGTCAAAGAGGTCATGAATTAAGGCTTGCAACTTTTTTCAAAAAAAAAAAAAAAAAA

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FIGURE 426

MGVWLNKDDYIRDLKRIILCFLIVYMAILVGTDQDFYSLLGVSKTASSREIRQAFKKLALKLH
PDKNPNNPNAHGDFLKINRAYEVLKDEDLRKKYDKYGEKLEDNQGGQYESWNYRYDFGIYD
DDPEIITLERREFDAAVNSGELWVFNFYSPGCSHCHDLAPTWRDFAKEVDGLLRIGAVNCGDD
RMLCRMKGVNPSYPSLFIFRSGMAPVKYHGDRSKESLVSFAMQHVRSTVTELWTGNFVNSIQTA
FAAGIGWLITFCSKGGDCLTSQTRLRLSGMLFLNSLDAKEIYLEVIHNLPDFELLSANTLEDR
LAHHRWLLFFHFGKNENSNDPELKKLKTLLKNDHIQVGRFDCSSAPDICSNLYVFQPSLAVFK
GQGTKEYEIHGKKILYDILAFAKESVNSHVTTLGPQNFPANDKEPWLVDFFAPWCPPCRALL
PELRRASNLLYGQLKFGTLDCTVHEGLCNMYNIQAYPTTVVFNQSNIEYEGHHSAEQILEFI
EDLMNPSVSVSLPTTTFNELVTQRKHNEVWMVDFYSPWCHPCQVLMPEWKRMARTLTGLINVGS
IDCQQYHSFCAQENVQRYPEIRFFPPKSNKAYQYHSYNGWNRDAYSLRIWGLGFLPQVSTDLT
PQTFSEKVLQGNHWVIDFYAPWCGPCQNFAPEFELLARMIKGKVKAGKVDCQAYAQTCQKAG
IRAYPTVKFYFYERAKRNFQEEQINTRDAKAIAALISEKLETLRNQGKRNKDEL

Important features:**Endoplasmic reticulum targeting sequence.**

amino acids 744-747

Cytochrome c family heme-binding site signature.

amino acids 158-163

Nt-dnaJ domain signature.

amino acids 77-96

N-glycosylation site.

amino acids 484-487

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FIGURE 427

CTGCAGTCAGGACTCTGGGACCGCAGGGGGCTCCCGGACCCTGACTCTGCAGCCGAACCGGCA
CGGTTTCGTGGGGACCCAGGCTTGCAAAGTGACGGTCATTTTCTCTTTCTTTCTCCCTCTTGA
GTCCTTCTGAGATGATGGCTCTGGGCGCAGCGGGAGCTACCCGGGTCTTTGTGCGGATGGTAG
CGGCGGCTCTCGGCGGCCACCCTCTGCTGGGAGTGAGCGCCACCTTGAACCTCGGTTCTCAATT
CCAACGCTATCAAGAACCTGCCCCACCGCTGGGCGGCGCTGCGGGGCACCCAGGCTCTGCAG
TCAGCGCCGCGCCGGGAATCCTGTACCCGGGCGGGAATAAGTACCAGACCATTGACAACCTACC
AGCCGTACCCGTGCGCAGAGGACGAGGAGTGCGGCACTGATGAGTACTGCGCTAGTCCCACCC
GCGGAGGGGACGCAGGCGTGCAAATCTGTCTCGCCTGCAGGAAGCGCCGAAAACGCTGCATGC
GTCACGCTATGTGCTGCCCCGGGAATTACTGCAAAAATGGAATATGTGTGTCTTCTGATCAAA
ATCATTTCCGAGGAGAAATTGAGGAAACCATCACTGAAAGCTTTGGTAATGATCATAGCACCT
TGGATGGGTATTCCAGAAGAACCACCTTGTCTTCAAAAATGTATCACACCAAAGGACAAGAAG
GTTCTGTTTGTCTCCGGTCATCAGACTGTGCCTCAGGATTGTGTTGTGCTAGACACTTCTGGT
CCAAGATCTGTAAACCTGTCCTGAAAGAAGGTCAAGTGTGTACCAAGCATAGGAGAAAAGGCT
CTCATGGACTAGAAATATTCCAGCGTTGTTACTGTGGAGAAGGTCTGTCTTGCCGGATACAGA
AAGATCACCATCAAGCCAGTAATTCTTCTAGGCTTCACACTTGTGAGAGACACTTAAACCAGCT
ATCCAAATGCAGTGAACCTCTTTTATATAATAGATGCTATGAAAACCTTTTATGACCTTCATC
AACTCAATCCTAAGGATATACAAGTTCTGTGGTTTCAGTTAAGCATTCCAATAACACCTTCCA
AAAACCTGGAGTGTAAGAGCTTTGTTTCTTTATGGAACTCCCCTGTGATTGCAGTAAATTACT
GTATTGTAAATTCTCAGTGTGGCACTTACCTGTAAATGCAATGAAACTTTTAATTATTTTTCT
AAAGGTGCTGCACTGCCTATTTTTCCTCTTGTTATGTAAATTTTGTACACATTGATTGTTAT
CTTGACTGACAAATATTCTATATTGAACTGAAGTAAATCATTTTCAGCTTATAGTTCTTAAAAG
CATAACCCTTTACCCCATTTAATTCTAGAGTCTAGAACGCAAGGATCTCTTGGAATGACAAAT
GATAGGTACCTAAAATGTAAATGAAAATACTAGCTTATTTTCTGAAATGTACTATCTTAATG
CTTAAATTATATTTCCCTTTAGGCTGTGATAGTTTTTGAAATAAAATTTAACATTTAAAAAAA
AAAAAA

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FIGURE 428

MMALGAAGATRVFVAMVAAALGGHPLLGVSATLNSVLNSNAIKNLPPPLGGAAGHPGSAVSAA
PGILYPGGNKYQTIDNYQPYPCAEDEECGTDEYCASPTRGGDAGVQICLACRKRRKRCMRHAM
CCPGNYCKNGICVSSDQNHFRGEIEETITESFGNDHSTLDGYSRRTLSSKMYHTKGQEGSVC
LRSSDCASGLCCARHFWSKICKPVLKEGQVCTKHRRKGSHGLEIFQRCYCGEGLSCRIQKDDH
QASNSSRLHTCQRH

Important features:**Signal peptide:**

amino acids 1-23

N-glycosylation site.

amino acids 256-259

Fungal Zn(2)-Cys(6) binuclear cluster domain

amino acids 110-126

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FIGURE 429

GAGAGGACGAGGTGCCGCTGCCTGGAGAATCCTCCGCTGCCGTCCGCTCCCGGAGCCCAGCCC
TTTCCTAACCCAACCCAACCTAGCCCAGTCCCAGCCGCCAGCGCCTGTCCCTGTCACGGACCC
CAGCGTTACCA**ATG**CATCCTGCCGTCTTCCTATCCTTACCCGACCTCAGATGCTCCCTTCTGCT
CCTGGTAACTTGGGTTTTTACTCCTGTAACAACCTGAAATAACAAGTCTTGCTACAGAGAATAT
AGATGAAATTTTAAACAATGCTGATGTTGCTTTAGTAAATTTTATGCTGACTGGTGTCTGTTT
CAGTCAGATGTTGCATCCAATTTTGGAGGAAGCTTCCGATGTCATTAAGGAAGAATTTCCAAA
TGAAATCAAGTAGTGTTTGCCAGAGTTGATTGTGATCAGCACTCTGACATAGCCCAGAGATA
CAGGATAAGCAAATACCCAACCCTCAAATTGTTTCGTAATGGGATGATGATGAAGAGAGAATA
CAGGGGTCAGCGATCAGTGAAAGCATTGGCAGATTACATCAGGCAACAAAAAGTGACCCCAT
TCAAGAAATTCGGGACTTAGCAGAAATCACCCTCTTGATCGCAGCAAAAGAAATATCATTGG
ATATTTTGAGCAAAAGGACTCGGACAACCTATAGAGTTTTTGAACGAGTAGCGAATATTTTGCA
TGATGACTGTGCCTTTCTTTCTGCATTTGGGGATGTTTCAAACCGGAAAGATATAGTGGCGA
CAACATAATCTACAAACCACAGGGCATTTCTGCTCCGGATATGGTGTACTTGGGAGCTATGAC
AAATTTTGATGTGACTTACAATTGGATTCAAGATAAATGTGTTCCCTCTTGTCCGAGAAATAAC
ATTTGAAAATGGAGAGGAATTGACAGAAGAAGGACTGCCTTTTCTCATACTCTTTCACATGAA
AGAAGATACAGAAAGTTTAGAAATATTCCAGAATGAAGTAGCTCGGCAATTAATAAGTGAAAA
AGGTACAATAAACTTTTTACATGCCGATTGTGACAAATTTAGACATCCTCTTCTGCACATACA
GAAAACCTCCAGCAGATTGTCCTGTAATCGCTATTGACAGCTTTAGGCATATGTATGTGTTTGG
AGACTTCAAAGATGTATTAATTCCTGGAAAACCTCAAGCAATTGATTTGACTTACATTCTGG
AAAACCTGCACAGAGAATTCCATCATGGACCTGACCCAACCTGATACAGCCCCAGGAGAGCAAGC
CCAAGATGTAGCAAGCAGTCCACCTGAGAGCTCCTTCCAGAACTAGCACCCAGTGAATATAG
GTATACTCTATTGAGGGATCGAGATGAGCTTT**TAA**AACTTGAAAAACAGTTTGTAAGCCTTTC
AACAGCAGCATCAACCTACGTGGTGGAAATAGTAAACCTATATTTTCATAATTCTATGTGTAT
TTTTATTTTGAATAAACAGAAAGAAATTTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
AAAAAAAAAAAA

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FIGURE 430

MHPAVFLSLPDLRCSLLLLVTWVFTPVTTEITSLATENIDEILNNADVALVNFYADWCRFSQM
LHPIFEEASDVIKEEFPNENQVVVFARVDCDQHS DIAQRYRISKYPTLKLFRNGMMMKREYRGQ
RSVKALADYIRQQKSDPIQEIRDLAEITTLDRSKRNIIGYFEQKSDNYRVFERVANILHDDC
AFLSAFGDVSKPERYSGDNIIYKPPGHSAPDMVYLGAMTNFDVTYNW IQDKCVPLVREITFEN
GEELTEEGLPFLILFHMKEDTESLEIFQNEVARQLISEKGTINFLHADCDKFRHPLLHIQKTP
ADCPVIAIDSRHMYVFGDFKDVLI PGKLKQFVFDLHSGKLHREFHHGPDPTDTAPGEQAQDV
ASSPPESSEFQKLAPSEYRYTLLRDRDEL

Important features:**Signal peptide:**

amino acids 1-29

Endoplasmic reticulum targeting sequence.

amino acids 403-406

Tyrosine kinase phosphorylation site.

amino acids 203-211

Thioredoxin family proteins

amino acids 50-66

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FIGURE 431

GAGCAGGACGGAGCCATGGACCCCGCCAGGAAAGCAGGTGCCCAGGCCATGATCTGGACTGCA
GGCTGGCTGCTGCTGCTGCTGCTTCGCGGAGGAGCGCAGGCCCTGGAGTGCTACAGCTGCGTG
CAGAAAGCAGATGACGGATGCTCCCCGAACAAGATGAAGACAGTGAAGTGCGCGCCGGGCGTG
GACGTCTGCACCGAGGCCGTGGGGGCGGTGGAGACCATCCACGGACAATTCTCGCTGGCAGTG
CGGGGTTGCGGTTTCGGGACTCCCCGGCAAGAATGACCGCGGCCTGGATCTTCACGGGCTTCTG
GCGTTCATCCAGCTGCAGCAATGCGCTCAGGATCGCTGCAACGCCAAGCTCAACCTCACCTCG
CGGGCGCTCGACCCGGCAGGTAATGAGAGTGCATACCCGCCCAACGGCGTGGAGTGCTACAGC
TGTGTGGGCCTGAGCCGGGAGGCGTGCCAGGGTACATCGCCGCCGGTTCGTGAGCTGCTACAAC
GCCAGCGATCATGTCTACAAGGGCTGCTTCGACGGCAACGTCACCTTGACGGCAGCTAATGTG
ACTGTGTCCTTGCCCTGTCCGGGGCTGTGTCCAGGATGAATTCTGCACTCGGGATGGAGTAACA
GGCCCAGGGTTCACGCTCAGTGGCTCCTGTTGCCAGGGGTCCCGCTGTAACCTCTGACCTCCGC
AACAAGACCTACTTCTCCCCTCGAATCCCACCCCTTGTCCGGCTGCCCCCTCCAGAGCCACG
ACTGTGGCCTCAACCACATCTGTCACCACTTCTACCTCGGCCCCAGTGAGACCCACATCCACC
ACCAAACCCATGCCAGCGCCAACCAGTCAGACTCCGAGACAGGGAGTAGAACACGAGGCCTCC
CGGGATGAGGAGCCCAGGTTGACTGGAGGCGCCGCTGGCCACCAGGACCGCAGCAATTCAGGG
CAGTATCCTGCAAAAGGGGGGGCCCCAGCAGCCCCATAATAAAGGCTGTGTGGCTCCACAGCT
GGATTGGCAGCCCTTCTGTTGGCCGTGGCTGCTGGTGTCTACTGTGAGCTTCTCCACCTGGA
AATTTCCCTCTCACCTACTTCTCTGGCCCTGGGTACCCCTCTTCTCATCACTTCCTGTTCCCA
CCACTGGACTGGGCTGGCCAGCCCCTGTTTTTCCAACATTCCCCAGTATCCCCAGCTTCTGC
TGCGCTGGTTTGC GGCTTTGGGAAATAAAATACCGTTGTATATATTCTGCCAGGGGTGTTCTA
GCTTTTTGAGGACAGCTCCTGTATCCTTCTCATCCTTGTCTCTCCGCTTGTCTCTTGTGATG
TTAGGACAGAGTGAGAGAAGTCAGCTGTCACGGGGAAGGTGAGAGAGAGGATGCTAAGCTTCC
TACTCACTTTCTCCTAGCCAGCCTGGACTTTGGAGCGTGGGGTGGGTGGGACAATGGCTCCCC
ACTCTAAGCACTGCCTCCCCTACTCCCCGCATCTTTGGGGAATCGGTTCCCCATATGTCTTCC
T TACTAGACTGTGAGCTCCTCGAGGGGGGGCCCGGTACCCAATTGCCCCTATAGTGAGTCGTA

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FIGURE 432

MDPARKAGAQAMIWTAGWLLLLLLRGGAQALECYSCVQKADDGCSPNKMKTVKCAPGVDVCTE
AVGAVETIHGQFSLAVRGCGSGLPGKNDRGLDLHGLLAFIQQQCAQDRCNAKLNLTSRALDP
AGNESAYPPNGVECYSCVGLSREACQGTSPPVVSCYNASDHVYKGCFDGNVTLTAANVTVSLP
VRGCVQDEFCTRDGVTGPGFTLSGSCCQGSRCNSDLRNKTYFSPRIPLVRLPPPEPTTVAST
TSVTTSTSAVRPTSTTKPMPAPTSQTPRQVEHEASRDEEPRLTGGAAGHQDRSNSGQYPAK
GGPQQPHNKGCVAPTAGLAALLLAVAAGVLL

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FIGURE 433

CGGGACTCGGCGGGTCCTCCTGGGAGTCTCGGAGGGGACCGGCTGTGCAGACGCC**ATG**GAGTT
GGTGCTGGTCTTCTCTGCAGCCTGCTGGCCCCCATGGTCCTGGCCAGTGCAGCTGAAAAGGA
GAAGGAAATGGACCCTTTTCATTATGATTACCAGACCCTGAGGATTGGGGGACTGGTGTTCGC
TGTGGTCCTCTTCTCGGTTGGGATCCTCCTTATCCTAAGTCGCAGGTGCAAGTGCAGTTTCAA
TCAGAAGCCCCGGGCCCCAGGAGATGAGGAAGCCCAGGTGGAGAACCTCATCACCGCCAATGC
AACAGAGCCCCAGAAGCAGAGAACTGAAGTGCAGCCATCAGGTGGAAGCCTCTGGAACCTGAG
GCGGCTGCTTGAACCTTTGGATGCAAATGTCGATGCT**TAA**GAAAACCGGCCACTTCAGCAACA
GCCCTTTCCCCAGGAGAAGCCAAGAACTTGTGTGTCCCCACCCTATCCCCTCTAACACCATT
CCTCCACCTGATGATGCAACTAACACTTGCCCTCCCCACTGCAGCCTGCGGTCTGCCCACCTC
CCGTGATGTGTGTGTGTGTGTGTGTGTGTGACTGTGTGTGTTTGCTAACTGTGGTCTTTGTGG
CTACTTGTTTGTGGATGGTATTGTGTTTGTAGTGAAGTGTGGACTCGCTTTCCCAGGCAGGG
GCTGAGCCACATGGCCATCTGCTCCTCCCTGCCCCGTGGCCCTCCATCACCTTCTGCTCCTA
GGAGGCTGCTTGTTGCCCCGAGACCAGCCCCCTCCCCTGATTTAGGGATGCGTAGGGTAAGAGC
ACGGGCAGTGGTCTTCAGTCGTCTTGGGACCTGGGAAGGTTTGCAGCACTTTGTCATCATTCT
TCATGGACTCCTTTTCACTCCTTTAACAAAAACCTTGCTTCCCTTATCCCACCTGATCCCAGTCT
GAAGGTCTCTTAGCAACTGGAGATACAAAGCAAGGAGCTGGTGAGCCCAGCGTTGACGTCAGG
CAGGCTATGCCCTTCCGTGGTTAATTTCTTCCAGGGGCTTCCACGAGGAGTCCCCATCTGCC
CCGCCCCCTTCACAGAGCGCCCGGGGATTCCAGGCCAGGGCTTCTACTCTGCCCTGGGGGAAT
GTGTCCCCTGCATATCTTCTCAGCAATAACTCCATGGGCTCTGGGACCCTACCCCTTCCAACC
TTCCCTGCTTCTGAGACTTCAATCTACAGCCCAGCTCATCCAGATGCAGACTACAGTCCCTGC
AATTGGGTCTCTGGCAGGCAATAGTTGAAGGACTCCTGTTCCGTTGGGGCCAGCACACCGGGA
TGGATGGAGGGAGAGCAGAGGCCTTTGCTTCTCTGCCTACGTCCCCTTAGATGGGCAGCAGAG
GCAACTCCCGCATCCTTTGCTCTGCCTGTGCGTGGTCAGAGCGGTGAGCGAGGTGGGTGGAG
ACTCAGCAGGCTCCGTGCAGCCCTTGGGAACAGTGAGAGGTTGAAGGTCATAACGAGAGTGGG
AACTCAACCCAGATCCCGCCCCCTCCTGTCCTCTGTGTTCCCGCGGAAACCAACCAACCGTGC
GCTGTGACCCATTGCTGTTCTCTGTATCGTGATCTATCCTCAACAACAACAGAAAAAAGGAAT
AAAATATCCTTTGTTTCCT

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FIGURE 434

MELVLVFLCSLLAPMVLASAAEKEKEMDPFHYDYQTLRIGGLVFAVVLFSVGILLIILSRCKC
SFNQKPRAPGDDEEAQVENLITANATEPQKQRTevQPSGGSLWNLRRLLLEPLDANVDA

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FIGURE 435

GGTCCTTA**ATG**GCAGCAGCCGCCGCTACCAAGATCCTTCTGTGCCTCCCGCTTCTGCTCCTGC
TGTCCGGCTGGTCCCGGGCTGGGCGAGCCGACCCTCACTCTCTTTGCTATGACATCACCGTCA
TCCCTAAGTTCAGACCTGGACCACGGTGGTGTGCGGTTCAAGGCCAGGTGGATGAAAAGACTT
TTCTTCACTATGACTGTGGCAACAAGACAGTCACACCTGTCAGTCCCCTGGGGAAGAACTAA
ATGTCACAACGGCCTGGAAAGCACAGAACCCAGTACTGAGAGAGGTGGTGGACATACTTACAG
AGCAACTGCGTGACATTCAGCTGGAGAATTACACACCCAAGGAACCCCTCACCTGCAGGCCAA
GGATGTCTTGTGAGCAGAAAGCTGAAGGACACAGCAGTGGATCTTGGCAGTTCAGTTTCGATG
GGCAGATCTTCCTCCTCTTTGACTCAGAGAAGAGAATGTGGACAACGGTTCATCCTGGAGCCA
GAAAGATGAAAGAAAAGTGGGAGAATGACAAGGTTGTGGCCATGTCCTTCCATTACTTCTCAA
TGGGAGACTGTATAGGATGGCTTGAGGACTTCTTGATGGGCATGGACAGCACCCCTGGAGCCAA
GTGCAGGAGCACCACTCGCCATGTCCTCAGGCACAACCCAACTCAGGGGCCACAGCCACCACCC
TCATCCTTTGCTGCCTCCTCATCATCCTCCCCTGCTTCATCCTCCCTGGCATCTGAGGAGAGT
CCTTTAGAGTGACAGGTTAAAGCTGATACCAAAGGCTCCTGTGAGCACGGTCTTGATCAAAC
TCGCCCTTCTGTCTGGCCAGCTGCCCACGACCTACGGTGTATGTCCAGTGGCCTCCAGCAGAT
CATGATGACATCATGGACCCAATAGCTCATTCACTGCCTTGATTCCCTTTTGCCAACAATTTTA
CCAGCAGTTATACCTAACATATTATGCAATTTTCTCTTGGTGCTACCTGATGGAATTCCTGCA
CTTAAAGTTCTGGCTGACTAAACAAGATATATCATTTTCTTTCTTCTCTTTTGTGGAAAA
TCAAGTACTTCTTTGAATGATGATCTCTTTCTTGCAAATGATATTGTCAGTAAAATAATCACG
TTAGACTTCAGACCTCTGGGGATTCTTTCCGTGTCCTGAAAGAGAATTTTAAATTATTTAAT
AAGAAAAAATTTATATTAATGATTGTTTCCTTTAGTAATTTATTGTTCTGTACTGATATTTAA
ATAAAGAGTTCTATTTCCCAAAAAAAAAAAAAAAAAA

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FIGURE 436

MAAAAATKILLCLPLLLLLSGWSRAGRADPHSLCYDITVIPKFRPGPRWCAVQGQVDEKTFH
YDCGNKTVTPVSPLGKKLNVTTAWKAQNPVLREVVDILTEQLRDIQLENYTPKEPLTLQARMS
CEQKAEGHSSGSWQFSFDGQIFLLFDSEKRMWTTVHPGARKMKEKWENDKVVAMSFHYFSMGD
CIGWLEDFLMGMDSTLEPSAGAPLAMSSGTTQLRATATTLILCCLLIILPCFILPGI

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FIGURE 437

GTTCTCCTTTCCGAGCCAAAATCCCAGGCGATGGTGAATTATGAACGTGCCACACC**ATGA**AGCTCTTGTGGCAGG
TAACTGTGCACCACCACACCTGGAATGCCATCCTGCTCCCGTTTCGTCTACCTCACGGCGCAAGTGTGGATTCTGT
GTGCAGCCATCGCTGCTGCCGCCTCAGCCGGGGCCCCAGAACTGCCCCCTCCGTTTGCTCGTGCAGTAACCAGTTCA
GCAAGGTGGTGTGCACGCGCCGGGGCCTCTCCGAGGTCCCGCAGGGTATTCCCTCGAACACCCGGTACCTCAACC
TCATGGAGAACAACATCCAGATGATCCAGGCCGACACCTTCCGCCACCTCCACCACCTGGAGGTCTGCAGTTGG
GCAGGAACTCCATCCGGCAGATTGAGGTGGGGGCCTTCAACGGCCTGGCCAGCCTCAACACCTGGAGCTGTTTCG
ACAACTGGCTGACAGTCATCCCTAGCGGGGCCTTTGAATACCTGTCCAAGCTGCGGGAGCTCTGGCTTCGCAACA
ACCCCATCGAAAGCATCCCCTCTTACGCCTTCAACCGGGTGCCCTCCCTCATGCGCCTGGACTTGGGGGAGCTCA
AGAAGCTGGAGTATATCTCTGAGGGAGCTTTTGAGGGGCTGTTCAACCTCAAGTATCTGAACTTGGGCATGTGCA
ACATTAAAGACATGCCCAATCTCACCCCCCTGGTGGGGCTGGAGGAGCTGGAGATGTCAGGGAACCACTTCCCTG
AGATCAGGCCTGGCTCCTTCCATGGCCTGAGCTCCCTCAAGAAGCTCTGGGTCTGAACCTCACAGGTGAGCCTGA
TTGAGCGGAATGCTTTTGACGGGCTGGCTTCACTTGTGGAACCTCAACTTGGCCACAATAACCTCTCTTCTTTGC
CCCATGACCTCTTTACCCCGCTGAGGTACCTGGTGGAGTTGCATCTACACCACAACCCTTGGAACTGTGATTGTG
ACATTCTGTGGCTAGCCTGGTGGCTTCGAGAGTATATACCCACCAATTCACCTGCTGTGGCCGCTGTCATGCTC
CCATGCACATGCGAGGCCGCTACCTCGTGGAGGTGGACCAGGCCTCCTTCCAGTGCTCTGCCCCCTTCATCATGG
ACGCACCTCGAGACCTCAACATTTCTGAGGGTTCGGATGGCAGAACTTAAGTGTGCGGACTCCCCCTATGTCTCCG
TGAAGTGGTTGCTGCCCAATGGGACAGTGCTCAGCCACGCCTCCCGCCACCCAAGGATCTCTGTCTCAACGACG
GCACCTTGAACCTTTTCCACGTGCTGCTTTCAGACACTGGGGTGTACACATGCATGGTGACCAATGTTGCAGGCA
ACTCCAACGCCTCGGCCTACCTCAATGTGAGCACGGCTGAGCTTAACACCTCCAACCTACAGCTTCTTACCACAG
TAACAGTGGAGACCACGGAGATCTCGCCTGAGGACACAACGCGAAAAGTACAAGCCTGTTCTACCACGTCCACTG
GTTACCAGCCGGCATATACCACCTCTACCACGGTGCTCATTGAGACTACCCGTGTGCCCAAGCAGGTGGCAGTAC
CCGCGACAGACACCACTGACAAGATGCAGACCAGCCTGGATGAAGTCATGAAGACCACCAAGATCATCATTGGCT
GCTTTGTGGCAGTGACTCTGCTAGCTGCCGCCATGTTGATTGTCTTCTATAAACTTCGTAAGCGGCACACGAGC
GGAGTACAGTCACAGCCGCCCGGACTGTTGAGATAATCCAGGTGGACGAAGACATCCAGCAGCAACATCCGCAG
CAGCAAACAGCAGCTCCGTCCGGTGTATCAGGTGAGGGGGCAGTAGTGCTGCCACAATTTCATGACCATATTAAC
ACAACACCTACAAACCAGCACATGGGGCCCACTGGACAGAAAAACAGCCTGGGGAACCTCTCTGCACCCACAGTCA
CCACTATCTCTGAACCTTATATAATTCAGACCCATACCAAGGACAAGGTACAGGAACTCAAATAT**TGA**CTCCCCT
CCCCCAAAAACTTATAAAATGCAATAGAATGCACACAAAGACAGCAACTTTTGTACAGAGTGGGGAGAGACTTT
TTCTTGTATATGCTTATATATTAAGTCTATGGGCTGGTTAAAAAAAACAGATTATATTAATAATTTAAAGACAAAA
AGTCAAAACA

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FIGURE 438

MKLLWQVTVHHHTWNAILLPFVYLTAQVWILCAAIAAAASAGPQNCPSVCSCSNQFSKVVCTR
RGLSEVPQGIPSNTRYLNLMENNIQMIQADTFRHLHHLEVLQLGRNSIRQIEVGAFNGLASLN
TLELFDNWLTVIPSGAFEYLSKLRRLWLRNNPIESIPSYAFNRVPSLMRLDLGELKKLEYISE
GAFEGLFNLKYLNLMCNIKDMPNLTPLVGLEELEMNGHNFPEIRPGSFHGLSSLKKLWVMNS
QVSLIERNAFDGLASLVELNLAHNNLSSLPHDLFTPLRYLVELHLHNPWNCDILWLAWWL
REYIPTNSTCCGRCHAPMHMRGRYLVEVDQASFQCSAPFIMDAPRDLNISEGRMAELKCRTPP
MSSVKWLLPNGTVLSHASRHPRI SVLNDGTLNFSHVLLSDTGVYTCMVTNVAGNSNASAYLNV
STAE LNTSNYSFFTTVTVETTEISPEDTTRKYKPVPTTSTGYQPAYTTSTTVLIQTTRVPKQV
AVPATD TTDKMQTS LDEVMKTTKIIIGCFVAVTLLAAAMLIVFYKLRKRHQQRSTVTAARTVE
IIQVDEDI PAATSAAATAAPSGVSGEGAVVLPTIHDHINYNTYKPAHGAHW TENS LGNSLHPT
VTTISEPYIIQTHTKDKVQETQI

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FIGURE 439

GTCGAATCCAAATCACTCATTGTGAAAGCTGAGCTCACAGCCGAATAAGCCACCATGAGGCTG
TCAGTGTGTCTCCTGATGGTCTCGCTGGCCCTTTGCTGCTACCAGGCCCATGCTCTTGTCTGC
CCAGCTGTTGCTTCTGAGATCACAGTCTTCTTATTCTTAAGTGACGCTGCGGTAAACCTCCAA
GTTGCCAAACTTAATCCACCTCCAGAAGCTCTTGCAGCCAAGTTGGAAGTGAAGCACTGCACC
GATCAGATATCTTTTAAGAAACGACTCTCATTGAAAAAGTCCTGGTGGAAATAGTAAAAAAT
GTGGTGTGTGACATGTAAAAATGCTCAACCTGGTTTCCAAAGTCTTTCAACGACACCCTGATC
TTCATAAAAAATTGTAAAGGTTTCAACACGTTGCTTTAATAAATCACTTGCCCTGC

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FIGURE 440

MRLSVCLLMVSLALCCYQAHALVCPAVASEITVFLFLSDAAVNLQVAKLNPPPEALAAKLEVK
HCTDQISFKKRLSLKKSWWK

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FIGURE 441

GAACATTTTTAGTTCCCAAGGAATGTACATCAGCCCCACGGAAGCTAGGCCACCTCTGGGATG
GGGTTGCTGGTTTAAAACAAACGCCAGTCATCCTATATAAGGACCTGACAGCCACCAGGCACC
ACCTCCGCCAGGAACTGCAGGCCCCACCTGTCTGCAACCCAGCTGAGGCC**ATG**CCCCTCCCCAGG
GACCGTCTGCAGCCTCCTGCTCCTCGGCATGCTCTGGCTGGACTTGGCCATGGCAGGCTCCAG
CTTCCTGAGCCCTGAACACCAGAGAGTCCAGCAGAGAAAGGAGTCGAAGAAGCCACCAGCCAA
GCTGCAGCCCCGAGCTCTAGCAGGCTGGCTCCGCCCCGGAAGATGGAGGTCAAGCAGAAGGGGC
AGAGGATGAACTGGAAGTCCGGTTCAACGCCCCCTTTGATGTTGGAATCAAGCTGTCAGGGGT
TCAGTACCAGCAGCACAGCCAGGCCCTGGGGAAGTTTCTTCAGGACATCCTCTGGGAAGAGGC
CAAAGAGGCCCCAGCCGACAAG**TGA**TCGCCCACAAGCCTTACTCACCTCTCTAAGTTTAGA
AGCGCTCATCTGGCTTTTCGCTTGCTTCTGCAGCAACTCCCACGACTGTTGTACAAGCTCAGG
AGGCGAATAAATGTTCAAACCTGTA

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FIGURE 442

MPSPGTVCSLLLLGMLWLDLAMAGSSFLSPEHQRVQQRKESKKPPAKLQPRALAGWLRPEDGG
QAEGAEDELEVRFNAPFDVGIKLSGVQYQQHSQALGKFLQDILWEEAKEAPADKO

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FIGURE 443

CGGCCACAGCTGGCATGCTCTGCCTGATCGCCATCCTGCTGTATGTCCTCGTCCAGTACCTCG
TGAACCCCGGGGTGCTCCGCACGGACCCAGATGTCAAGAATATGAACACGTGGCTGCTGTTTC
CTCCCCCTGTTCCCGGTGCAGGTGCAGACCCTGATAGTCGTGATCATCGGGATGCTCGTGCTC
CTGCTGGACTTTCTTGGCTTGGTGCACCTGGGCCAGCTGCTCATCTTCCACATCTACCTGAGT
ATGTCCCCCACCCTAAGCCCCCGATCCCCCAAGGCTGGGTGGTCAGAGCTGCTCATCTTACA
CCTCTACTTGAGTATGTCCCTAACCCTGAGCCCCCACGCCTGGGGCCAGAGTCTTTGTCCCC
CGTGTGCGCATGTGTTTCAGGGTCAGCCTCTCCCAGAAAGTGAGATCATGGACAAAAAGGGCAAA
TCACAGGAAGAAATTAAATCCATGAGGACCCAGCAGGCCAGCAAGAAGCTGAACTCACGCCG
AGACCTGCAGGAGTGGTGCCAGGTGCTTGAAGTAACAAGTTTAAAATGTTTCAGAGACAATGGA
ATGGAATCTATTAGGCAAGAACAGGACATTATGAAATAAGGACAGGTGGACTTCCAAAAACAC
AAGTAGAAATTCTAACAATGAAATATATTACAGGCAGGTCACCCACTAACCAAACTGAAG
CGAGAGCTGTGGTCTTGCTTGGTCTCACAGTGGGCACAGCGGTAGGCGGTGAGTCATGTTGCT
GAACGACGGAGGGTAAACTCCCCAGCCCCAAGAAAACCTGTGTTGGAAGTAACAACAACCTCC
CTGCTCCTGGCACCAGCCGTTTTGGTTCATGGTGGGCCAGCTGCAAAGCGTCTTCCATTCTCTG
GGCAGTGGTGGCCCCGAGGCTGTGGCCTCTCAGGGGGTTTTCTGTGGACACGGGCAGCAGAGTG
TGTCCAGGCCAGCCCCAAGAATGCCCTGCTCCTGACAGCTTGGCCAACCCCTGGTCAGGGCA
GAGGGAGTTGGGTGGGTTCAGGCTCTGGGCTCACCTCCATCTCCAGAGCATCCCCTGCCTGCAG
TTGTGGCAAGAACGCCCAGCTCAGAATGAACACACCCCCACCAAGAGCCTCCTTGTTTCATAACC
ACAGGTTACCCTACAAACCACTGTCCCCACACAACCCTGGGGATGTTTTTAAACACACACCTC
TAACGCATATCTTACAGTCACTGTTGTCTTGCCTGAGGGTTGAATTTTTTTTAAATGAAAGTGC
AATGAAAATCACTGGATTAAATCCTACGGACACAGAGCTGAAAAAAAAAAAAAAAAAAAAA
AAAAAAAAA

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FIGURE 444

MNTWLLFLPLFPVQVQTLIVVIIGMLVLLLDLGLVHLGQLLI FHIYLSMSPTLS PRSPQGWV
VRAAHLTPLLEYVPNPEPPTPGARVFVPRVRMCSGSASPRSEIMDKKGKSQEEIKSMRTQQAQ
QEAELTPRPAGVVPGA

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FIGURE 445

AGGCGGGCAGCAGCTGCAGGCTGACCTTGCAGCTTGGCGGAATGGACTGGCCTCACAACCTGC
TGTTTCTTCTTACCATTTCCATCTTCCTGGGGCTGGGCCAGCCCAGGAGCCCCAAAAGCAAGA
GGAAGGGGCAAGGGCGGCCTGGGCCCCCTGGCCCCTGGCCCTCACCAGGTGCCACTGGACCTGG
TGTCACGGATGAAACCGTATGCCCCGATGGAGGAGTATGAGAGGAACATCGAGGAGATGGTGG
CCCAGCTGAGGAACAGCTCAGAGCTGGCCCAGAGAAAGTGTGAGGTCAACTTGCAGCTGTGGA
TGTCCAACAAGAGGAGCCTGTCTCCCTGGGGCTACAGCATCAACCACGACCCCAGCCGTATCC
CCGTGGACCTGCCGGAGGCACGGTGCCTGTGTCTGGGCTGTGTGAACCCCTTCACCATGCAGG
AGGACCGCAGCATGGTGAGCGTGCCGGTGTTTCAGCCAGGTTCCCTGTGCGCCGCCGCCTCTGCC
CGCCACCGCCCCGCACAGGGCCTTGCCGCCAGCGCGCAGTCATGGAGACCATCGCTGTGGGCT
GCACCTGCATCTTCTGAATCACCTGGCCCAGAAGCCAGGCCAGCAGCCGAGACCATCCTCCT
TGCACCTTTGTGCCAAGAAAGGCCTATGAAAAGTAAACACTGACTTTTGAAAGCAAG

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FIGURE 446

MDWPHNLLFLLTISIFLGLGQPRSPKSKRKGQGRPGPLAPGPHQVPLDLVSRMKPYARMEEYE
RNIEMVAQLRNSSELAQRKCEVNLQLWMSNKRSLSPWGYSINHDPRI PVDLPEARCLCLGC
VNPFTMQEDRSMVSVPVFSQVPVRRRLCPPPPRTGPCRQRAVMETIAVGCTCIF

Important features:**Signal peptide:**

amino acids 1-20

N-glycosylation site.

amino acids 75-78

Homologous region to IL-17

amino acids 96-180.

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FIGURE 447

GGAGTGCAGATGGCATCCTTCGGTTCTTCCAGACAAGCTGCAAGACGCTGACCATGGGCCAAGA
TGGAGCTCTCGAAGGCCTTCTCTGGCCAGCGGACACTCCTATCTGCCATCCTCAGCATGCTAT
CACTCAGCTTCTCCACAACATCCCTGCTCAGCAACTACTGGTTTGTGGGCACACAGAAGGTGC
CCAAGCCCCTGTGCGAGAAAGGTCTGGCAGCCAAGTGCTTTGACATGCCAGTGTCCTTGGATG
GAGATACCAACACATCCACCCAGGAGGTGGTACAATACTGGGAGACTGGGGATGACCGGT
TCTCCTTCCGGAGCTTCCGGAGTGGCATGTGGCTATCCTGTGAGGAACTGTGGAAGAACCAG
GGGAGAGGTGCCGAAGTTTCATTGAACTTACACCACCAGCCAAGAGAGGTGAGAAAGGACTAC
TGGAATTTGCCACGTTGCAAGGCCCATGTCACCCCACTCTCCGATTTGGAGGGAAGCGGTTGA
TGGAGAAGGCTTCCCTCCCCCTCCCCCTCCCTTGGGGCTTTGTGGCAAAAATCCTATGGTTATCC
CTGGGAACGCAGATCACCTACATCGGACTTCAATTCATCAGCTTCCTCCTGCTACTAACAGAC
TTGCTACTCACTGGGAACCCTGCCTGTGGGCTCAAAGTGGAGCGCCTTTGCTGCTGTTTCCTCT
GTCCTGTCAGGTCTCCTGGGGATGGTGGCCACATGATGTATTCACAAGTCTTCCAAGCGACT
GTCAACTTGGGTCCAGAAGACTGGAGACCACATGTTTGAATTATGGCTGGGCCTTCTACATG
GCCTGGCTCTCCTTCACCTGCTGCATGGCGTCGGCTGTCAACCACCTTCAACACGTACACCAGG
ATGGTGCTGGAGTTCAAGTGCAAGCATAGTAAAGAGCTTCAAGGAAAACCCGAAGTGCCTACCA
CATCACCATCAGTGTTTCCCTCGGCGGCTGTCAAGTGCAGCCCCCACCCTGGGGTCCTTTGACC
AGCTACCACCAGTATCATAATCAGCCCATCCACTCTGTCTCTGAGGGAGTCGACTTCTACTCC
GAGCTGCGGAACAAGGGATTTCAAAGAGGGGGCCAGCCAGGAGCTGAAAGAAGCAGTTAGGTCA
TCTGTAGAGGAAGAGCAGTGTTAGGAGTTAAGCGGGTTTGGGGAGTAGGCTTGAGCCCTACCT
TACACGTCTGCTGATTATCAACATGTGCTTAAGCCAACATCCGTCTCTTGAGCATGGTTTTTTA
GAGGCTACGAATAAGGCTATGAATAAGGGTTATCTTTAAGTCCTAAGGGATTCTTGGGTGCCA
CTGCTCTCTTTTCTCTACAGCTCCATCTTGTTTCACCCACCCACATCTCACACATCCAGAA
TTCCCTTCTTTACTGATAGTTTCTGTGCCAGGTCTGGGCTAAACCATGGAGATAAAAAGAAG
AGTAAAATACACTTCCCGACCTTAAGGATCTGAAA

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FIGURE 448

MAKMELSKAFSGQRTLLSAILSMLSLSFSTTSLLSNYWFVGTQKVPKPLCEKGLAAKCFDMPV .
SLDGDNTNTSTQEVVQYNWETGDDRFSSFRSFRSGMWLSCEETVEEPGERCRSFIELTPPAKRGE
KGLLEFATLQGPCHPTLRFGGKRLMEKASLSPPLGLCGKNPMVIPGNADHLHRTSIHQLP
TNRLATHWEPCLWAQTERLCCCFLCPVRSPGDGGPHDVFTSLPSDCQLGSRRLCTTCLELWLG
LLHGLALLHLLHGVGCHHLQHVHQDGAGVQVQA

FIGURE 449

CCACACGCGTCCGCCACACGCTCCGCCACACGCGTCCGCCACACGCGTCCGCCACACGCGTCCGCCACACGCGTCCGCC
ACGCGTCCCGGTGCAAGCTCCGCCCGCACACTGCTGGTGGAGGGAAGGAGCCCGGGCGCCTCTCGCCGCTCCCGC
CGCCGCGCTCCGCACTCCCCACCGCCCGCCCGCCCGCCCGCCCGCCGCAAGCATGAGTGAGCCGCTCTCT
GCAGCTGCCCGGGGCGGAATGGCAGGCTGTTTCCGCCGAGTAAAAGGTGGCGCCGCTCAGTGGTCTGTTTCCAAT
GACGGACATTAACAGACTGTAGATCTCTGGGAGTCCGCGAGCCCGAGTTTGGAGTTTTCCTCCCCCAACAGCT
CAGACTCCGAATCCAGAGGGAAAGGAGCGGAGGAGGCGAAGCGTCTGGGCTCCGCGACGTAGTTGGAAACT
TGCGGGTCTAGAAGTTCGCTCCCCGCTTGGCGGCCGCCCTTGCAGCCCCGAGCCGAGCAGCAAAGTGAGACAT
TGTGCGCTGCCAGATCCGCCGCCCGGACCGGGGCTGCTCGGAAACACAGAGGGGTCTTCTCTCGCCCTGCA
TATAATTAGCTGCACAAAGGAGCAGCTGAATGGAGTTGTCTACTCTTGAAAAAGGATTTCTGACCGAGCG
CTTCCAATTGGACATTTCCAGTCTCTTGAAAGATTCTCGCTAATGGATTTCCTGCTGCTCGGTCTCTGTCTAT
ACTGGCTGCTGAGGAGGCCCTCGGGGTTGGTCTTGTGTCTGCTGGGGGCTGCTTCAGATGCTGCCCGCGCC
CCAGCGGGTGCCCGCAGCTGTGCCGTGCGAGGGCGGCTGCTATGCGAGCGCTCAACCTACCGAGGGCG
CCCAACAACCTGTCCGGCTGCTGGCTGTCTCTGCGTACAAACAGCTCTCGGAGCTGCGCGCCGGCCAGTCA
CGGGGTTAATGCAGCTCAGCTGGCTCTATCTGGATACAAATCACATCTGCTCCGTGCAGGGGGACGCCCTTCAGA
AACTGCGCCGAGTTAAGAACTCAGCTGAGTTCCAACAGATACCCAACTGCCAACACCACTTCGGGCCCA
TGCCAAACCTGCGCAGCTGGACTCTCGTACAAACAGCTGAGGCGCTGCGCGCCGACCTCTCCACGGGCTGC
GGAAGCTCACCACGCTGCATATGCGGGCCAAACGCAATCCAGTTTGTGCCGTGCGCATCTCCAGGACTGCCGA
GCTCAAGTTTCTGCATCGGATACATACAGTCAAGAGTCTGGCGCGCAACTCTTCGCGGCTTGTTTAAGT
TACCGAGCTGCACCTCGAGCACACAGACTTTGGTCAAGGTGAACCTCGCCACTTCGCGCGCTCATCTCCCTGC
ACTCGCTCTGCTGCGGAGGAACAAGGTGGCCATTGTGGTACGTGCTGGACTGGGTGGTGAACCTGGAGAAAA
TGGACTTGTGGGCAACGAGATCGATACATGAGGCCCCATGTGTTGAGACCGTGCCGACCTGCAGTCCCTGC
AGCTGGACTCCAACGCCCTCACTACATCGAGCCCGGATCTCAACTCTTGAAGTCCCTGACAAGCATCACCC
TGGCCGGGAACCTGTGGGATTGCGGGCGCAACGTGTGTGCCCTAGCTCGTGGCTGCAACATCCAGGGGCGCT
ACGATGGCAACTTCAGTGCGCAGCCCGAGTAGCAGGCGAGGACGTCCTGGACGCGCTGATCGCCTTCC
ACCTGTGCGAGGATGGGGCGAGCCACACGCGGCCACTGCTCTCGGCGTACCAACCGCAGTGATCTGGGC
CCCCTGCCAGCTCGGCCACACGCTCGCGGACGCGGGGAGGGGCGAGCAGCAGGCGCATCTCGAGCCTGCCACG
TGGCTCTTCCAGGCGGAGCAGCGCCGAGAACGCGGTGCAGATCCAAAGTGGTCAAGGCACTTCCAGGCACTTCC
CTTCTCCTTCTCATCGTGGTCTGTGCTTACGTGCTCGTGAAGTGTTCAGCCAGCCTCAGGCAGCTCA
GACAGTGCTTTGTACGCAGCGCAGGAAGCAAAAGCAGAAACAGACCATGCATCAGATGGCTGCCATGTCTGCC
AGGAATACTACGTGATTGACAAAGCAACCAATGAGGGAGCCCTGGTGATCATCAACAGTATGGCTCGTGTA
CTTGCCACACGAGCCCGCAGAGGAAATGCGAGTTGTAATGTGCTCCAGCTGGCTCAACCCATCGCTACCAATA
CGCCTGGGCAGCCGGGACGGGCGGGCGGGCACAGGCTGGGGTCTCCTTGTCTGTGCTCTGATATGCTCCTTGAC
TGAAACTTTAAGGGGATCTCTCCAGAGACTTGACATTTAGCTTTATTTGTGCTCTTAAAAACAAAGCGAATTA
AACACACAAAAAAGCCCCACCCACAACTTGAGCAGCTCATCTTAAATTTATATGAGAATCCTCTCCCTCC
TTTGAAGATCTGTCCATATTCAGGAATCTGAGAGTGTAAGAAAGGTGGCCATAAGACAGAGAGAGAATAATCGTG
CTTTGTTTATATGCTACTCTCCACCCCTGCCCATGATTAACATCATGTATGTAGAAGTCTTAAGTCCATACG
ATTTTCATGAAGAACCAATTGGAAAGGAAATCTGCAATCTGGGAGCTTAAGAGCAAAATGATGACCATAGAAAGCTA
TGTTCTTACTTTGTGTGTGTGTCTGTATGTTCTGCGTGTGTGTCTTTGTAGGCAAGCAACGTTGTCTACACA
AACGGGAATTAGTCCATCATTTTCATGCCCCCTGTGCCCTAGCTCTGGAGATTGGTGGGGGAGGTGGGGGA
AACGGCAGGAATAGGGAAGGTGTAGTTTAACTAAGGTTTGTAAACATTGAAATCTTTTCTTCTCAAAATTA
ATTATCTTAAAGCTTCAAGAACTTGCTCTGACCCCTTAAGCAAACACTAAGCATTTAAAGAGAAATCTAATT
TTTAAAGGTGTAGCACTTTTCTTTTATCTTCCACAGAGGGTGCTAATCTATTGCTGTGCTATCTGAAAA
GAACTTAAGGCCACAATTCAGGTCTCGTCTGGGCAATTGTGATGGATTGACCTCCATTTGCAGTACCTCCGAG
CTGATTAAAGTTCAGCAGTGGTATTAGGTTTTTGAATATTTATATAGAAAAAAGTCTTTTACATGACAAAT
GACACTCTCACACAGCTTAGCCCTAGTAGTTTTTATAGTTGGACCAAGGAGGCTTAATGAGACCTGCTC
CTCTGCTGCACTCAGAAAAAATAGGCATCCGTGATGCTCAGATCTTAGCCTTGATATTAATAGTTGAGACCAC
TACCCACAATGCAGCCTATACTCCAAGACTACAAAGTTACCATCGCAAGAAAGGATTTATCCAGATAAAGGAA
ATAGTTTTCTCAACCATTTAAAAATATTTCTGAACATCAAGTAGAAGAGCCCCAACCTTTTCTCTGCTC
CTTCAAGAAGGCAGACATTTGTATGATTTAGCATCAACACACATTTATGAGTATATGTAAGTAATCAGAGGGG
CAAATGCCACTTGTATTCTCCAAAGTTTTTCAAGCAAGTACACACAGATCTCTGTGATGAGTATAGGGGCCACT
GTGTTTTCCGGCTTATTTTAGTCGACTTGTTCAGCAAGTTTGATGCTAGCTATCTGACATGGCCCCAGTAGACAG
GGCATTGATGATCATGAT
CCAGAAATATATCTGTTTTGGAGCAAGAGTGTATAATGTTTCAGGGTAGTCAAAATAACATAAATATCTCC
TATGATGAGTGGCGGATGTTGGCTGATTTGGGCTGCCATTGACAGAAATGCAAAATAAAGGAATTAGCTAGAA
TGTAGACCAATTAATGTGCTTTGAAATATATTTTGAATAGGTTTGAATGTCA

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FIGURE 450

MDFLLLGLCLYWLLRRPSGVVLCLLGACFQMLPAAPSGCPQLCRCEGRLLYCEALNLTEAPHN
LSGLLGLSLRYNSLSELRAGQFTGLMQLTWLYLDHNNHICSVQGDAFQKLRRVKELTLSSNQIT
QLPNTTFRPMPNLRSDLSYNKLQALAPDLFHGLRKLTTLHMRANAIQFVPVRIFQDCRSLKF
LDIGYNQLKSLARNSFAGLFKLTEHLEHNDLVKVNFAHFPRLISLHSLCLRRNKVAIVVSSL
DWVWNLEKMDLSGNEIEYMEPHVFETVPHLQSLQLDSNRLTYIEPRIILNSWKSLSITLAGNL
WDCGRNVCALASWLSNFQGRYDGNLQCASPEYAQGEDVLDVYAFHLCEDGAEPTSGHLLSAV
TNRSDLGPPASSATTADGGEGQHDGTFEPATVALPGGEHAENAVQIHKVVTGTMALIFSFLI
VVLVLYVSWKCFPASLRQLRQCFVTQRRKQKQKQTMHQMAAMSAQEYYVDYKPNHIEGALVII
NEYGSCTCHQQPARECEV

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FIGURE 451

TTGAGCGCAGGTGAGCTCCTGCGCGTTCCGGGGGCGTTCCTCCAGTCACCCTCCCGCCGTTAC
CCGCGGCGCGCCCCGAGGGAGTCTCCTCCAGACCCTCCCTCCCGTTGCTCCAACTAATACGGA
CTGAACGGATCGCTGCGAGGGTGGGAGAGAAAATTAGGGGGAGAAAGGACAGAGAGAGCAACT
ACCATCCATAGCCAGATAGATTATCTTACACTGAACTGATCAAGTACTTTGAAA**ATG**ACTTCG
AAATTTATCTTGGTGTCTTCATACTTGCTGCACTGAGTCTTTCAACCACCTTTTCTCTCCAA
CTAGACCAGCAAAAGGTTCTACTAGTTTCTTTTGATGGATTCCGTTGGGATTACTTATATAAA
GTTCCAACGCCCCATTTTCATTATATTATGAAATATGGTGTTCACGTGAAGCAAGTTACTAAT
GTTTTTATTACAAAAACCTACCCTAACCATTATACTTTGGTAACTGGCCTCTTTGCAGAGAAT
CATGGGATTGTTGCAAATGATATGTTTGATCCTATTTCGGAACAAATCTTTCTCCTTGGATCAC
ATGAATATTTATGATTCCAAGTTTTGGGAAGAAGCGACACCAATATGGATCACAAACCAGAGG
GCAGGACATACTAGTGGTGCAGCCATGTGGCCCGGAACAGATGTAAAAATACATAAGCGCTTT
CCTACTCATTACATGCCTTACAATGAGTCAGTTTCATTTGAAGATAGAGTTGCCAAAATTGTT
GAATGGTTTACGTCAAAAGAGCCCATAAATCTTGGTCTTCTCTATTGGGAAGACCCTGATGAC
ATGGGCCACCATTGTTGGGACCTGACAGTCCGCTCATGGGGCCTGTCAATTCAGATATTGACAAG
AAGTTAGGATATCTCATACAAATGCTGAAAAAGGCAAAGTTGTGGAACACTCTGAACCTAATC
ATCACAAGTGATCATGGAATGACGCAGTGCTCTGAGGAAAGGTTAATAGAAGTTGACCAGTAC
CTGGATAAAGACCACTATAACCCTGATTGATCAATCTCCAGTAGCAGCCATCTTGCCAAAAGAA
GGTAAATTTGATGAAGTCTATGAAGCACTAACTCACGCTCATCCTAATCTTACTGTTTACAAA
AAAGAAGACGTTCCAGAAAGGTGGCATTACAAATACAACAGTCGAATTCACCAATCATAGCA
GTGGCTGATGAAGGGTGGCACATTTTACAGAATAAGTCAGATGACTTTCTGTTAGGCAACCAC
GGTTACGATAATGCGTTAGCAGATATGCATCCAATATTTTTAGCCCATGGTCCCTGCCTTCAGA
AAGAATTTCTCAAAAGAAGCCATGAACTCCACAGATTTGTACCCACTACTATGCCACCTCCTC
AATATCACTGCCATGCCACACAATGGATCATTCGGAATGTCCAGGATCTGCTCAATTCAGCA
ATGCCAAGGGTGGTCCCTTATACACAGAGTACTATACTCCTCCCTGGTAGTGTTAAACCAGCA
GAATATGACCAAGAGGGGTACATACCCTTATTTCATAGGGGTCTCTCTTGGCAGCATTATAGTG
ATTGTATTTTTTGTAAATTTTCATTAAGCATTTAATTCACAGTCAAATACCTGCCTTACAAGAT
ATGCATGCTGAAATAGCTCAACCATTATTACAAGCC**TAA**TGTTACTTTGAAGTGGATTGTCAT
ATTGAAGTGGAGATTCCATAATTATGTCAGTGTTTAAAGGTTTCAAATTCCTGGGAAACCAGTT
CCAAACATCTGCAGAAACCATTAAGCAGTTACATATTTAGGTATACACACACACACACACA
CACATACACACACACGGACCAAAATACTTACACCTGCAAAGGAATAAAGATGTGAGAGTATGT
CTCCATTGTTCACTGTAGCATAGGGATAGATAAGATCCTGCTTTATTTGGACTTGGCGCAGAT
AATGTATATATTTAGCAACTTTGCACTATGTAAAGTACCTTATATATTGCACTTTAAATTTCT
CTCCTGATGGGTACTTTAATTTGAAATGCACTTTATGGACAGTTATGTCTTATAACTTGATTG
AAAATGACAACTTTTTTGACCCCATGTACAGAAATACTTGTTACGCATTGTTCAAACCTGAAGGA
AATTTCTAATAATCCCGAATAATGAACATAGAAATCTATCTCCATAAATTGAGAGAAGAAGAA
GGTGATAAGTGTGAAAATTAAATGTGATAACCTTTGAACCTTGAATTTTGGAGATGTATTCC
CAACAGCAGAATGCAACTGTGGGCATTTCTTGTCTTATTTCTTTCCAGAGAACGTGGTTTTCA
TTTATTTTTTCCCTCAAAAGAGAGTCAAATACTGACAGATTCGTTCTAAATATATTGTTTCTGT
CATAAAATTATTGTGATTTCTGATGAGTCATATTACTGTGATTTTCATAATAATGAAGACAC
CATGAATATACTTTTTCTTCTATATAGTTTCAAGCAATGGCCTGAATAGAAGCAACCAGGCACCAT
CTCAGCAATGTTTTCTTGTGTTTGTAAATTATTTGCTCCTTTGAAAATTAAATCACTATTAATT
ACATTAAAAATCAAATTGGATAAAAAAAAAAAAAAAAAAAAAA

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FIGURE 452

MTSKFILVSFILAALSLSTTFSLQLDQQKVLLVSFDGFRWDYLYKVPTPHFHYIMKYGVHVKQ
VTNVFITKTYPNHYTLVTGLFAENHGIVANDMFDPIRNKSFSLDHMNIYDSKFWEEATPIWIT
NQRAGHTSGAAMWPGTDVKIHKRFPTHYMPYNESVSFEDRVAKIVEWFTSKEPINLGLLYWED
PDDMGHHLGPDSPLMGPVISDIDKKLGYLIQMLKKAKLWNTLNLIITSDHGMTQCSEERLIEL
DQYLDKDHYTELIDQSPVAAILPKEGKFDEVYEALTHAHPNLTVYKKEDVPERWHYKYNSRIQP
IIA VADEGWHLQNKSDDFLLGNHGYDNALADMHPIFLAHGPAFRKNFSKEAMNSTDLYPLLC
HLLNITAMPHNGSFWNVQDLLNSAMPRVVPYTQSTILLPGSVKPAEYDQEGSYPYFIGVSLGS
IIIVIVFFVIFIKHLIHSQIPALQDMHAEIAQPLLQA

Important features:**Signal Peptide:**

amino acids 1-22

Transmembrane Domain:

amino acids 429-452

N-glycosylation sites:amino acids 101-104, 158-161, 292-295, 329-332, 362-365, 369-372,
382-385, 389-392**Somatomedin B Domain:**

amino acids 69-85

Sulfatase protein Region:

amino acids 212-241

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FIGURE 454

MAPQSLPSSRMAPLGMLLGLLMAACFTFCLSHQNLKEFALTNPESSTKETERKETKAEEELD
AEVLEVFHPTHEWQALQPGQAVPAGSHVRLNLQTGEREAKLQYEDKFRNNLKGKRLDINTNTY
TSQDLKSALAKFKEGAEMESSKEDKARQAEVKRLFRPIEELKKDFDELNVVIETDMQIMVRLI
NKFNSSSSSLEEKIAALFDLEYVHQMDNAQDLLSFGGLQVVINGLNSTEPLVKEYAAFVLGA
AFSSNPKVQVEAIEGGALQKLLVILATEQPLTAKKKVLFALCSLLRHFPYAQRQFLKLGGGLQV
LRTLQVEKGTEVLAVRVVTLTYDLVTEKMFAEEEAELTQEMSPEKLQQYRQVHLLPGLWEQGW
CEITAHLLALPEHDAREKVLQTLGVLLTTCRDRYRQDPQLGRTLASLQAEYQVLASLELQDGE
DEGYFQELLGSVNSLLKELR

Important features:**Signal peptide:**

amino acids 1-29

Hypothetical YJL126w/YLR351c/yhcX family protein.

amino acids 364-373

N-glycosylation site.

amino acids 193-197, 236-240

N-myristoylation site.

amino acids 15-21, 19-25, 234-240, 251-257, 402-408, 451-457

Homologous region SLS1 protein.

amino acids 68-340

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FIGURE 455

GCCCCAGGGAGCAGTGGGTGGTTATAACTCAGGCCCCGGTGCCCAGAGCCCAGGAGGAGGCAGT
GGCCAGGAAGGCACAGGCCTGAGAAGTCTGCGGCTGAGCTGGGAGCAAATCCCCACCCCCTA
CCTGGGGGACAGGGCAAGTGAGACCTGGTGAGGGTGGCTCAGCAGGCAGGGAAGGAGAGGTGT
CTGTGCGTCCTGCACCCACATCTTTCTCTGTCCCCTCCTTGCCCTGTCTGGAGGCTGCTAGAC
TCCTATCTTCTGAATTCTATAGTGCCTGGGTCTCAGCGCAGTGCCGATGGTGGCCCGTCCTTG
TGGTTCCTCTCTACCTGGGGAAATAAGGTGCAGCGGCCATGGCTACAGCAAGACCCCCCTGGA
TGTGGGTGCTCTGTGCTCTGATCACAGCCTTGCTTCTGGGGGTACAGAGCATGTTCTCGCCA
ACAATGATGTTTCTGTGACCACCCCTCTAACACCGTGCCCTCTGGGAGCAACCAGGACCTGG
GAGCTGGGGCCGGGGAAGACGCCCCGGTCGGATGACAGCAGCAGCCGCATCATCAATGGATCCG
ACTGCGATATGCACACCCAGCCGTGGCAGGCCGCGCTGTTGCTAAGGCCCAACCAGCTCTACT
GCGGGGCGGTGTTGGTGCATCCACAGTGGCTGCTCACGGCCGCCACTGCAGGAAGAAAGTTT
TCAGAGTCCGTCTCGGCCACTACTCCCTGTCACCAGTTTATGAATCTGGGCAGCAGATGTTCC
AGGGGGTCAAATCCATCCCCACCCCTGGCTACTCCACCCCTGGCCACTCTAACGACCTCATGC
TCATCAAACCTGAACAGAAGAATTTCGTCCCCTAAAGATGTCAGACCCATCAACGTCTCCTCTC
ATTGTCCCTCTGCTGGGACAAAGTGCTTGGTGTCTGGCTGGGGGACAACCAAGAGCCCCCAAG
TGCACCTCCCTAAGGTCCTCCAGTGCTTGAATATCAGCGTGCTAAGTCAGAAAAGGTGCGAGG
ATGCTTACCCGAGACAGATAGATGACACCATGTTCTGCGCCGGTGACAAAGCAGGTAGAGACT
CCTGCCAGGGTGATTCTGGGGGGCCTGTGGTCTGCAATGGCTCCCTGCAGGGACTCGTGTCT
GGGGAGATTACCCTTGTGCCCCGGCCCAACAGACCGGGTGTCTACACGAACCTCTGCAAGTTCA
CCAAGTGATCCAGGAAACCATCCAGGCCAACTCCTTGAGTCATCCCAGGACTCAGCACACCGG
CATCCCCACCTGCTGCAGGGACAGCCCTGACACTCCTTTCAGACCCTCATTCCTTCCCAGAGA
TGTTGAGAATGTTTCATCTCTCAGCCCCTGACCCCATGTCTCCTGGACTCAGGGTCTGCTTCC
CCCACATTGGGCTGACCGTGTCTCTAGTTGAACCCTGGGAACAATTTCCAAAACCTGTCCAG
GGCGGGGGTTGCGTCTCAATCTCCCTGGGGCACTTTCATCCTCAAGCTCAGGGCCCATCCCTT
CTCTGCAGCTCTGACCCAAATTTAGTCCCAGAAATAAACTGAGAAGTGGAACCAAAAAA

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FIGURE 456

MATARPPWMWVLCALITALLLGVTEHVLANNDVSCDHPSNTVPSGSNQDLGAGAGEDARSDDS
SSRIINGSDCDMHTQPWQAALLLRPNQLYCGAVLVHPQWLLTAAHCRKKVFRVRLGHYSLSPV
YESGQQMFQGVKSIHPHGYSHPGHSNDLMLIKLNRIRPTKDVRPINVSSHCP SAGTKCLVSG
WGTTKSPQVHF PKVLQCLNISVLSQKRCE DAYPRQIDDTMFCAGDKAGRDSCQGD SGGPVVCN
GSLQGLVSWGDYPCARPNRPGVYTNLCKFTKWIQETIQANS

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FIGURE 457

GCAGTCAGAGACTTCCCCTGCCCCCTCGCTGGGAAAGAACATTAGGAATGCCTTTTAGTGCCCTTGCTTCCTGAACT
AGCTCACAGTAGCCCCGGCGGCCAGGGCAATCCGACCACATTTCACTCTCACCGCTGTAGGAATCCAGATGCAGG
CCAAGTACAGCAGCACGAGGGACATGCTGGATGATGATGGGGACACCACCATGAGCCTGCATTCTCAAGCCTCTG
CCACAACCTCGGCATCCAGAGCCCCGGCGCACAGAGCACAGGGCTCCCTCTTCAACGTGGCGACCAGTGGCCCTGA
CCCTGCTGACTTTGTGCTTGGTGCTGCTGATAGGGCTGGCAGCCCTGGGGCTTTTGTTCAGTACTACCAGC
TCTCCAATACTGGTCAAGACACCATTTCTCAAATGGAAGAAAGATTAGGAAATACGTCCCAAGAGTTGCAATCTC
TTCAAGTCCAGAATATAAAGCTTGCAGGAAGTCTGCAGCATGTGGCTGAAAACTCTGTCTGAGCTGTATAACA
AAGCTGGAGCACACAGGTGCAGCCCTTGTACAGAACAATGGAAATGGCATGGAGACAATTGCTACCAGTTCTATA
AAGACAGCAAAAGTTGGGAGGACTGTAAATATTTCTGCCTTAGTGAAAACTCTACCATGCTGAAGATAAACAAAC
AAGAAGACCTGGAATTTGCCGCGTCTCAGAGCTACTCTGAGTTTTTCTACTCTTATTGGACAGGGCTTTTGCGCC
CTGACAGTGGAAGGCCCTGGCTGTGGATGGATGGAACCCCTTTCACTTCTGAACTGTTCCATATTATAATAGATG
TCACCAGCCCAAGAAGCAGAGACTGTGTGGCCATCCTCAATGGGATGATCTTCTCAAAGGACTGCAAAGAATTGA
AGCGTTGTGTCTGTGAGAGAAGGGCAGGAATGGTGAAGCCAGAGAGCCTCCATGTCCCCCTGAAACATTAGGCG
AAGGTGACTTGATTCGCCCTCTGCAACTACAAATAGCAGAGTGAGCCAGGCGGTGCCAAAGCAAGGGCTAGTTGAG
ACATTGGGAAATGGAACATAATCAGGAAAGACTATCTCTCTGACTAGTACAAAATGGGTTCTCGTGTTTCCTGTT
CAGGATCACCAGCATTTCTGAGCTTGGGTTTATGCACGTATTTAACAGTCACAAGAAGTCTTATTTACATGCCAC
CAACCAACCTCAGAAACCCATAATGTCATCTGCCTTCTTGGCTTAGAGATAACTTTTAGCTCTCTTTCTTCTCAA
TGTCTAATATCACCTCCCTGTTTTTCATGTCTTCCTTACACTTGGTGGAATAAGAACTTTTTGAAGTAGAGGAAA
TACATTGAGGTAACATCCTTTCTCTGACAGTCAAGTAGTCCATCAGAAATTGGCAGTCACTTCCCAGATTGTAC
CAGCAAATACACAAGGAATTCTTTTTGTTTGTTCAGTTCATACTAGTCCCTTCCCAATCCATCAGTAAAGACCC
CATCTGCCTTGTCCATGCCGTTTCCCAACAGGGATGTCACTTGATATGAGAATCTCAAATCTCAATGCCTTATAA
GCATTCCCTTCTGTGTCCATTAAGACTCTGATAATTGTCTCCCCCTCCATAGGAATTTCTCCAGGAAAGAAATAT
ATCCCCATCTCCGTTTCATATCAGAACTACCGTCCCCGATATTCCCTTCAGAGAGATTAAAGACCAGAAAAAAGT
GAGCCTCTTCATCTGCACCTGTAATAGTTTCAGTTCCTATTTTCTTCCATTGACCCATATTTATACCTTTCAGGT
ACTGAAGATTTAATAATAATAAATGTAAATACTGTGAAAAA

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FIGURE 458

MQAKYSSTRDMLDDDGD TTMSLHSQASATTRHPEPRRTEHRAPSSTWRPVALTLLTLCLVLLI
GLAALGLLFFQYYQLSNTGQDTISQMEERLGNTSQELQSLQVQNIKLAGSLQHVAEKLCRELY
NKAGAHRCSPCTEQWKWHGDNCYQFYKDSKSWEDCKYFCLSENSTMLKINKQEDLEFAASQSY
SEFFYSYWTGLLRPDSGKAWLWMDGTPFTSELFHIIIDVTSPRSRDCVAILNGMIFSKDCKEL
KRCVCERRAGMVKPESLHVPPETLGEGD

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FIGURE 459

GTTGATGGCAAACCTTCCTCAAAGGAGGGGCAGAGCCTGCGCAGGGCAGGAGCAGCTGGCCCCAC
TGGCGGGCCCCGCAACACTCCGTCTCACCCCTCTGGGCCCCACTGCATCTAGAGGAGGGCCGTCTGT
GAGGCCACTACCCCTCCAGCAACTGGGAGGTGGGACTGTCAGAAGCTGGCCCCAGGGTGGTGGT
CAGCTGGGTCAGGGACCTACGGCACCTGCTGGACCACCTCGCCTTCTCCATCGAAGCAGGGAA
GTGGGAGCCTCGAGCCCTCGGGTGGAAGCTGACCCCAAGCCACCCTTCACCTGGACAGGATGA
GAGTGTGAGGTGTGCTTCGCCTCCTGGCCCTCATCTTTGCCATAGTCACGACATGGATGTTTA
TTCGAAGCTACATGAGCTTCAGCATGAAAACCATCCGTCTGCCACGCTGGCTGGCAGCCTCGC
CCACCAAGGAGATCCAGGTTAAAAAGTACAAGTGTGGCCTCATCAAGCCCTGCCCAGCCAACT
ACTTTGCGTTTAAAATCTGCAGTGGGGCCGCCAACGTCGTGGGCCCTACTATGTGCTTTGAAG
ACCGCATGATCATGAGTCCTGTGAAAAACAATGTGGGCAGAGGCCTAAACATCGCCCTGGTGA
ATGGAACCACGGGAGCTGTGCTGGGACAGAAGGCATTTGACATGTACTCTGGAGATGTTATGC
ACCTAGTGAAATTCCTTAAAGAAATTCCGGGGGGTGCACTGGTGCTGGTGGCCTCCTACGACG
ATCCAGGGACCAAAATGAACGATGAAAGCAGGAAACTCTTCTCTGACTTGGGGAGTTTCCTACG
CAAAACAACCTGGGCTTCCGGGACAGCTGGGTCTTCATAGGAGCCAAAGACCTCAGGGGTAAAA
GCCCCCTTTGAGCAGTTCTTAAAGAACAGCCCAGACACAAACAAATACGAGGGATGGCCAGAGC
TGCTGGAGATGGAGGGCTGCATGCCCCCGAAGCCATTTTAGGGTGGCTGTGGCTCTTCCTCAG
CCAGGGGCCTGAAGAAGCTCCTGCCTGACTTAGGAGTCAGAGCCCGGCAGGGGCTGAGGAGGA
GGAGCAGGGGGTGCTGCGTGGAAGGTGCTGCAGGTCTTGCACGCTGTGTGCGCCTCTCCTC
CTCGGAAACAGAACCCCTCCCACAGCACATCCTACCCGGAAGACCAGCCTCAGAGGGTCCTTCT
GGAACCAGCTGTCTGTGGAGAGAATGGGGTGCTTTCGTCAGGGACTGCTGACGGCTGGTCCTG
AGGAAGGACAAACTGCCCAGACTTGAGCCCAATTAAATTTTATTTTGGCTGGTTTTGAAAAAA
AAAAAAAAAAAAAA

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FIGURE 460

MRVSGVLRLLALIFAIVTTWMFIRSYMSFSMKTIRLPRWLAASPTKEIQVKKYKCGLIKPCPA
NYFAFKICSGAANVVGPTMCFEDRMIMSPVKNNVGRGLNIALVNGTTGAVLGQKAFDMYSGDV
MHLVKFLKEIPGGALVLVASYYDDPGTKMNDESRKLFSDLGSSYAKQLGFRDSWVFIGAKDLRG
KSPFEQFLKNSPDTNKYEGWPELLEMEGCMPPKPF

Important features:**Signal peptide:**

amino acids 1-15

ATP/GTP-binding site motif A (P-loop).

amino acids 184-191

N-glycosylation site.

amino acids 107-110

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FIGURE 461

AAACTCAGCACTTGCCGGAGTGGCTCATTGTTAAGACAAAGGGTGTGCACTTCCTGGCCAGGA
AACCTGAGCGGTGAGACTCCCAGCTGCCTACATCAAGGCCCCAGGACATGCAGAACCTTCCTC
TAGAACCCGACCCACCACC**ATG**AGGTCTGCTGTGGAGATGCAGGCACCTGAGCCAAGGCGT
CCAGTGGTCCTTGCTTCTGGCTGTCCTGGTCTTCTTTCTCTTCGCCTTGCCCTCTTTTATTAA
GGAGCCTCAAACAAAGCCTTCCAGGCATCAACGCACAGAGAACATTAAAGAAAGGTCTCTACA
GTCCCTGGCAAAGCCTAAGTCCCAGGCACCCACAAGGGCGAGGAGGACAACCATCTATGCAGA
GCCAGCGCCAGAGAACAAATGCCCTCAACACACAAACCCAGCCCAAGGCCCACACCACCGGAGA
CAGAGGAAAGGAGGCCAACCAGGCACCGCCGGAGGAGCAGGACAAGGTGCCCCACACAGCACA
GAGGGCAGCATGGAAGAGCCCAGAAAAAGAGAAAACCATGGTGAACACACTGTCACCCAGAGG
GCAAGATGCAGGGATGGCCTCTGGCAGGACAGAGGCACAATCATGGAAGAGCCAGGACACAAA
GACGACCCAAGGAAATGGGGGCCAGACCAGGAAGCTGACGGCCTCCAGGACGGTGTGAGAGAA
GCACCAGGGCAAAGCGGCAACCACAGCCAAGACGCTCATTTCCCAAAGTCAGCACAGAATGCT
GGCTCCACAGGAGCAGTGTCAACAAGGACGAGACAGAAAGGAGTGACCACAGCAGTCATCCC
ACCTAAGGAGAAGAAACCTCAGGCCACCCACCCCTGCCCTTTCCAGAGCCCCACGACGCA
GAGAAACCAAAGACTGAAGGCCGCCAACTTCAAATCTGAGCCTCGGTGGGATTTTGAGGAAAA
ATACAGCTTCGAAATAGGAGGCCTTCAGACGACTTGCCCTGACTCTGTGAAGATCAAAGCCTC
CAAGTCGCTGTGGCTCCAGAACTCTTTCTGCCAACCTCACTCTCTTCTGGACTCCAGACA
CTTCAACCAGAGTGAGTGGGACCGCCTGGAACACTTTGCACCACCCTTTGGCTTCATGGAGCT
CAACTACTCCTTGGTGCAGAAGGTCGTGACACGCTTCCCTCCAGTGCCCCAGCAGCAGCTGCT
CCTGGCCAGCTCCCCGCTGGGAGCCTCCGGTGCATCACCTGTGCCGTGGTGGGCAACGGGGG
CATCCTGAACAACTCCCACATGGGCCAGGAGATAGACAGTCACGACTACGTGTTCCGATTGAG
CGGAGCTCTCATTAAAGGCTACGAACAGGATGTGGGGACTCGGACATCCTTCTACGGCTTTAC
CGCCTTCTCCCTGACCCAGTCACTCCTTATATTGGGCAATCGGGGTTTCAAGAACGTGCCTCT
TGGGAAGGACGTCCGCTACTTGCACTTCTGGAAGGCACCCGGGACTATGAGTGGCTGGAAGC
ACTGCTTATGAATCAGACGGTGATGTCAAAAAACCTTTTCTGGTTCAGGCACAGACCCCAGGA
AGCTTTTTCGGGAAGCCCTGCACATGGACAGGTACCTGTTGCTGCACCCAGACTTTCTCCGATA
CATGAAGAACAGGTTTCTGAGGTCTAAGACCCTGGATGGTGCCCACTGGAGGATATACCGCCC
CACCCTGGGGCCCTCCTGCTGCTCACTGCCCTTCAGCTCTGTGACCAGGTGAGTGCTTATGG
CTTCATCACTGAGGGCCATGAGCGCTTTTCTGATCACTACTATGATACATCATGGAAGCGGCT
GATCTTTTACATAAACCATGACTTCAAGCTGGAGAGAGAAGTCTGGAAGCGGCTACACGATGA
AGGGATAATCCGGCTGTACCAGCGTCCTGGTCCCAGGAACTGCCAAAGCCAAGAACT**TGA**CCGGG
GCCAGGGCTGCCATGGTCTCCTTGCTGCTCCAAGGCACAGGATACAGTGGGAATCTTGAGAC
TCTTTGGCCATTTCCCATGGCTCAGACTAAGCTCCAAGCCCTTCAGGAGTTCCAAGGGAACAC
TTGAACCATGGACAAGACTCTCTCAAGATGGCAAATGGCTAATTGAGGTTCTGAAGTTCTTCA
GTACATTGCTGTAGGTCCTGAGGCCAGGGATTTTAAATTAAATGGGGTGATGGGTGGCCAATA
CCACAATTCTGCTGAAAAACACTCTTCCAGTCCAAAAGCTTCTTGATACAGAAAAAAGAGCC
TGGATTTACAGAAACATATAGATCTGGTTTGAATTCCAGATCGAGTTTACAGTTGTGAAATCT
TGAAGGTATTACTTAACTTCACTACAGATTGTCTAGAAGACCTTTCTAGGAGTTATCTGATTC
TAGAAGGGTCTATACTTGTCTTGTCTTTAAGCTATTTGACAACCTCTACGTGTTGTAGAAAAAC
TGATAATAATACAAATGATTGTTGTCCATGGAAAGGCAAATAAATTTTCTACAGTGAAAAAA
AAAAAAA

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FIGURE 462

MRSCLWRCRHLSQGVQWSLLLAVLVFFLFALPSFIKEPQTKPSRHQRTENIKERSLQSLAKPK
SQAPTRARRTTIYAEPAPENNALNTQTQPKAHTTGDRGKEANQAPPEEQDKVPHTAQRAAWKS
PEKEKTMVNTLSPRGQDAGMASGRTEAQSWKSQDTKTTQGNGGQTRKLTASRTVSEKHQGKAA
TTAKTLIPKSQHRMLAPTGA VSTRTRQKGVTTAVIPPEKKPQATPPPAPFQSPTTQRNQRLK
AANFKSEPRWDFEEKYSFEIGGLQTTCPDSVKIKASKSLWLQKLFLPNLTLFLDSRHFNQSEW
DRLEHFAPPPFGFMELNYSLVQKVVTFRFPVPQQQLLLASLPAGSLRCITCAVVGNGGILNNSH
MGQEIDSHDYVFRLSGALIKGYEQDVGTRTSFYGFTAFTSLTQSLILGNRGFKNVPLGKDVRV
LHFLEGTRDYEWLEALLMNQTVMSKNLFWFRHRPQEAFFREALHMDRYLLLHPDFLRVMKNRFL
RSKTL'DGAHWRIYRPTTGALLLLTALQLCDQVSAYGFITEGHERFSDHYYDTSWKRLIFYINH
DFKLEREVWKRLHDEGIIRLYQRPGPGTAKAKN

Important features:**Cytoplasmic Domain:**

amino acids 1-10

Type II Transmembrane Domain:

amino acids 11-35

Lumenal catalytic Domain:

amino acids 36-600

Ribonucleotide Reductase small subunit Signature:

amino acids 481-496

N-glycosylation Sites:

amino acids 300-303, 311-314, 331-334, 375-378, 460-463

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FIGURE 463

GGGGGAGCTAGGCCGGCGGCAGTGGTGGTGGCGGCGGCGCAAGGGTGAGGGCGGCCCCAGAAC
CCCAGGTAGGTAGAGCAAGAAG**ATG**GTGTTTCTGCCCCCTCAAATGGTCCCTTGCAACCATGTC
ATTTCTACTTTTCTCACTGTTGGCTCTCTTAACTGTGTCCACTCCTTCATGGTGTGAGAGCAC
TGAAGCATCTCCAAAACGTAGTGATGGGACACCATTTCCTTGGAATAAAAATACGACTTCCTGA
GTACGTCATCCCAGTTCATTATGATCTCTTGATCCATGCAAACCTTACCACGCTGACCTTCTG
GGGAACCACGAAAGTAGAAATCACAGCCAGTCAGCCCACCAGCACCATCATCCTGCATAGTCA
CCACCTGCAGATATCTAGGGCCACCCTCAGGAAGGGAGCTGGAGAGAGGCTATCGGAAGAACC
CCTGCAGGTCTTGGAAACACCCCCCTCAGGAGCAAATTGCACTGCTGGCTCCCGAGCCCCCTCCT
TGTCGGGCTCCCGTACACAGTTGTCACTTCACTATGCTGGCAATCTTTCCGAGACTTTCCACGG
ATTTTACAAAAGCACCTACAGAACCAAGGAAGGGGAAGTGAAGGATACTAGCATCAACACAATT
TGAACCCACTGCAGCTAGAATGGCCTTTCCCTGCTTTGATGAACCTGCCTTCAAAGCAAGTTT
CTCAATCAAATTAGAAGAGAGCCAAGGCACCTAGCCATCTCCAATATGCCATTGGTGAAATC
TGTGACTGTTTGTGAAGGACTCATAGAAGACCATTTTGTATGTCACTGTGAAGATGAGCACCTA
TCTGGTGGCCTTCATCATTTTCAGATTTTGTGCTGTGAGCAAGATAACCAAGAGTGGAGTCAA
GGTTTCTGTTTATGCTGTGCCAGACAAGATAAATCAAGCAGATTATGCACTGGATGCTGCGGT
GACTCTTCTAGAATTTTATGAGGATTAATTTTCAGCATACCGTATCCCCCTACCCAAACAAGATCT
TGCTGCTATTTCCGACTTTTCAGTCTGGTGTCTATGGAAAACCTGGGACTGACAACATATAGAGA
ATCTGCTCTGTTGTTTGTATGCAGAAAAGTCTTCTGCATCAAGTAAGCTTGGCATCACAGTGAC
TGTGGCCCATGAACTGGCCCAACAGTGGTTTGGGAACCTGGTCACTATGGAATGGTGGAAATGA
TCTTTGGCTAAATGAAGGATTTGCCAAATTTATGGAGTTTGTGTCTGTCACTGTGACCCATCC
TGAAGTGAAGTTGGAGATTATTTCTTTGGCAAATGTTTTGACGCAATGGAGGTAGATGCTTT
AAATTCCTCACACCCTGTGTCTACACCTGTGGAAAACCTGCTCAGATCCGGGAGATGTTTGA
TGATGTTTCTTATGATAAGGGAGCTTGTATTCTGAATATGCTAAGGGAGTATCTTAGCGCTGA
CGCATTTAAAAGTGGTATTGTACAGTATCTCCAGAAGCATAGCTATAAAAATACAAAAAACGA
GGACCTGTGGGATAGTATGGCAAGTATTTGCCCTACAGATGGTGTAAAAGGGATGGATGGCTT
TTGCTCTAGAAGTCAACATTTCATCTTCATCCTCACATTGGCATCAGGAAGGGGTGGATGTGAA
AACCATGATGAACACTTGGACACTGCAGAGGGGTTTTCCCTAATAACCATCACAGTGAGGGG
GAGGAATGTACACATGAAGCAAGAGCACTACATGAAGGGCTGTGACGGCGCCCCGGACACTGG
GTACCTGTGGCATGTTCCATTGACATTCATCACAGCAAATCCAACATGGTCCATCGATTTTT
GCTAAAAACAAAACAGATGTGCTCATCCTCCCAGAAAGAGGTGGAATGGATCAAATTTAATGT
GGGCATGAATGGCTATTACATTGTGCATTACGAGGATGATGGATGGGACTCTTTGACTGGCCT
TTTAAAAGGAACACACAGCAGTCAAGCAAGTAAATGATCGGGCAAGTCTCATTAACAATGCATT
TCAGCTCGTCAGCAATTGGGAAGCTGTCCATTGAAAAGGCCTTGGATTTATCCCTGTACTTGAA
ACATGAAACTGAAATTATGCCCCTGTTTCAAGGTTTGAATGAGCTGATTCCCTATGTATAAGTT
AATGGAGAAAAGAGATATGAATGAAGTGGAAACTCAATTCAAGGCCTTCCTCATCAGGCTGCT
AAGGGACCTCATTTGATAAGCAGACATGGACAGACGAGGGCTCAGTCTCAGAGCAAATGCTGCG
GAGTGAACCTACTACTCCTCGCCTGTGTGCACAACATATCAGCCGTGCGTACAGAGGGCAGAAG
CTATTTTCAGAAAAGTGGAAAGGAATCCAATGGAAACTTGAGCCTGCCTGTGACGTGACCTTGGC
AGTGTGTTGCTGTGGGGGCCCCAGAGCACAGAAGGCTGGGATTTTCTTTATAGTAAATATCAGTT
TTCTTTGTCCAGTACTGAGAAAAGCCAAATTTGAATTTGCCCTCTGCAGAACCCAAAATAAGGA
AAAGCTTCAATGGCTACTAGATGAAAGCTTTAAGGGAGATAAAATAAAAACCTCAGGAGTTTCC
ACAAATTCTTACACTCATTGGCAGGAACCCAGTAGGATACCCACTGGCCTGGCAATTTCTGAG
GAAAAACTGGAACAAACTTGTACAAAAGTTTGAACCTTGGCTCATCTTCCATAGCCCACATGGT
AATGGGTACAACAAATCAATTCTCCACAAGAACACGGCTTGAAGAGGTAAAAGGATTCTTCAG
CTCTTTGAAAGAAAATGGTTCTCAGCTCCGTTGTGTCCAACAGACAATTGAAACCATTTGAAGA
AAACATCGGTTGGATGGATAAGAATTTTGATAAAATCAGAGTGTGGCTGCAAAGTGAAAAGCT
TGAACGTAT**GTA**AAATTCCTCCCTTGCCCGGTTCTGTTATCTCTAATCACCACATTTTGT
TGAGTGTATTTTCAAACCTAGAGATGGCTGTTTTGGCTCCAACCTGGAGATACTTTTTTCCCTTC
AACTCATTTTTTGTACTATCCCTGTGAAAAGAATAGCTGTTAGTTTTTTCATGAATGGGCTTTTT
CATGAATGGGCTATCGCTACCATGTGTTTTGTTTCATCACAGGTGTTGCCCTGCAACGTAAACC
CAAGTGTGGGTTCCCTGCCACAGAAGAATAAAGTACCTTATTTCTTCAAAAAAAAAAAAAA
AAAAAAAAAAAAA

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FIGURE 464

MVFLPLKWSLATMSFLLSSLLALLTVSTPSWCQSTEASPKRSDGTPFPWNKIRLPEYVIPVHY
DLLIHANLTTLTFWGTTKVEITASQPTSTIILHSHHLQISRATLRKGAGERLSEEPLQVLEHP
PQEQIALLAPEPLLVLGLPYTVVIHYAGNLSETFHGFYKSTYRTKEGELRILASTQFEPTAARM
AFPCFDEPAFKASF SIKIRREPRHLAISNMPLVKSVTVAEGLIEDHFDVTVKMSTYLVAFIIS
DFESVSKITKSGVKVSVYAVPDKINQADYALDAVTLLEFYEDYFSIPYPLPKQDLAAIPDFQ
SGAMENWGLTTYRESALLFDAEKSSASSKLGITVTVAHEL AHQWFGNLVTMEWWNDLWLN EGF
AKFMEFVSVSVTHPELKVG DYFFGKCFDAMEVDALNSSHPVSTPVENPAQIREMFDDVS YDKG
ACILNMLREYLSADAFKSGIVQYLQKHSYKNTKNEDLWDSMASICPTDG VKGMDGFC SRSQHS
SSSSHWHQEGVDVKTM MNTWTLQRGFPLITITVRGRNVHMKQEHYMKGSDGAPDTGYLWHVPL
TFITSKSNMVHRFLLKTKTDVLILPEEVEWIKFNVGMNGYYIVHYEDDGWDSL TGLLKGTHTA
VSSNDRASLINNAFQLV SIGKLSIEKALDLSLYLKHETEIMPVFQGLNELIPMYKLMEKRDMN
EVETQFKAFILIRLLRDLIDKQWTWDEGSVSEQMLRSELLLLACVHNYQPCVQRAEGYFRKWKE
SNGNLSLPVDVTLAVFAVGAQSTEGWDFLYSKYQFSLSTEKSQIEFALCRTQNKEKLQWLLD
ESFKGDKIKTQEFQP ILTILGRNPVGYPLAWQFLRKNWNKLVQKFELGSSSIAHMVMGTTNQF
STRTRLEEVKGFFSSLKENGSQLRCVQQT IETIEENIGWMDKNFDKIRVWLQSEKLERM

Important features:**Signal peptide:**

amino acids 1-34

N-glycosylation sites:

amino acids 70-74, 154-158, 414-418, 760-764, 901-905

Neutral zinc metallopeptidases, zinc-binding region signature:

amino acids 350-360

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FIGURE 465

CAGCCACAGACGGGTCATGAGCGCGGTATTACTGCTGGCCCTCCTGGGGTTCATCCTCCCCT
GCCAGGAGTGCAGGCGCTGCTCTGCCAGTTTGGGACAGTTCAGCATGTGTGGAAGGTGTCCGA
CCTACCCCGGCAATGGACCCCTAAGAACACCAGCTGCGACAGCGGCTTGGGGTGCCAGGACAC
GTTGATGCTCATTGAGAGCGGACCCCAAGTGAGCCTGGTGCTCTCCAAGGGCTGCACGGAGGC
CAAGGACCAGGAGCCCCGCGTCACTGAGCACCGGATGGGCCCCGGCCTCTCCCTGATCTCCTA
CACCTTCGTGTGCCGCCAGGAGGACTTCTGCAACAACCTCGTTAACTCCCTCCCGCTTTGGGC
CCCACAGCCCCCAGCAGACCCAGGATCCTTGAGGTGCCAGTCTGCTTGTCTATGGAAGGCTG
TCTGGAGGGGACAACAGAAGAGATCTGCCCCAAGGGGACCACACACTGTTATGATGGCCTCCT
CAGGCTCAGGGGAGGAGGCATCTTCTCCAATCTGAGAGTCCAGGGATGCATGCCCCAGCCAGG
TTGCAACCTGCTCAATGGGACACAGGAAATTGGGCCCCTGGGTATGACTGAGAACTGCAATAG
GAAAGATTTTCTGACCTGTCATCGGGGGACCACATTATGACACACGGAACTTGGCTCAAGA
ACCCACTGATTGGACCACATCGAATACCGAGATGTGCGAGGTGGGGCAGGTGTGTCAGGAGAC
GCTGCTGCTCATAGATGTAGGACTCACATCAACCCTGGTGGGGACAAAAGGCTGCAGCACTGT
TGGGGCTCAAAATTCCCAGAAGACCACCATCCACTCAGCCCCTCCTGGGGTGCTTGTGGCCTC
CTATACCCACTTCTGCTCCTCGGACCTGTGCAATAGTGCCAGCAGCAGCAGCGTTCTGCTGAA
CTCCCTCCCTCCTCAAGCTGCCCCCTGTCCCAGGAGACCGGCAGTGTCTACCTGTGTGCAGCC
CCTTGGAACCTGTTCAAGTGGCTCCCCCGAATGACCTGCCCCAGGGGCGCCACTCATTGTTA
TGATGGGTACATTATCTCTCAGGAGGTGGGCTGTCCACCAAATGAGCATTTCAGGGCTGCGT
GGCCCAACCTTCCAGCTTCTTGTTGAACCACACCAGACAAATCGGGATCTTCTCTGCGCGTGA
GAAGCGTGATGTGCAGCCTCCTGCCTCTCAGCATGAGGGAGGTGGGGCTGAGGGCCTGGAGTC
TCTCACTTGGGGGGTGGGGCTGGCACTGGCCCCAGCGCTGTGGTGGGGAGTGGTTTGCCCTTC
CTGCTTAACTCTATTACCCCCACGATTCTTCACCGCTGCTGACCACCCACACTCAACCTCCCTC
TGACCTCATAACCTAATGGCCTTGACACCAGATTCTTTCCATTCTGTCCATGAATCATCTT
CCCCACACACAATCATTATATCTACTCACCTAACAGCAACACTGGGGAGAGCCTGGAGCATC
CGGACTTGCCCTATGGGAGAGGGGACGCTGGAGGAGTGGCTGCATGTATCTGATAATACAGAC
CCTGTCCTTTCA

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FIGURE 466

MSAVLLLALLGFILPLPGVQALLCQFGTVQHVKVSDLPQWTPKNTSCDSGLGCQDTLMLIE
SGPQVSLVLSKGCTEAKDQEPRVTEHRMGPLSLISYTFVCRQEDFCNNLVNSLPLWAPQPPA
DPGSLRCPVCLSMEGCLEGTTEEICPKGTTHCYDGLLRRLRGGGIFSNLRVQGCMPQPGCNLLN
GTQEIGPVGMTENCNRKDFTLCHRGTTIMTHGNLAQEPTDWTTSNTEMCEVGQVCQETLLID
VGLTSTLVGTKGCSTVGAQNSQKTTIHSAPPGVLVASYTHFCSSDLCNSASSSSVLLNSLPPQ
AAPVPGDRQCPTCVQPLGTCSSGSPRMTCPRGATHCYDGYIHLGGGLSTKMSIQGCVAQPSS
FLLNHTRQIGIFSAREKRDVQPPASQHEGGGAEGLESLTWGVGLALAPALWWGVVCPSC

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FIGURE 467

GAGGATTTGCCACAGCAGCGGATAGAGCAGGAGAGCACCACCGGAGCCCTTGAGACATCCTTG
AGAAGAGCCACAGCATAAGAGACTGCCCTGCTTGGTGTGTTTTGCAGG**ATG**ATGGTGGCCCTTCG
AGGAGCTTCTGCATTGCTGGTTCTGTTTCCTTGCAGCTTTTCTGCCCCCGCCGCAGTGTACCCA
GGACCCAGCCATGGTGCATTACATCTACCAGCGCTTTCGAGTCTTGGAGCAAGGGCTGGAAAA
ATGTACCCAAGCAACGAGGGCATAACATTCAAGAATTCCAAGAGTTCTCAAAAAATATATCTGT
CATGCTGGGAAGATGTCAGACCTACACAAGTGAGTACAAGAGTGCAGTGGGTAACTTGGCACT
GAGAGTTGAACGTGCCCAACGGGAGATTGACTACATAACAATACCTTCGAGAGGCTGACGAGTG
CATCGTATCAGAGGACAAGACACTGGCAGAAATGTTGCTCCAAGAAGCTGAAGAAGAGAAAAA
GATCCGGACTCTGCTGAATGCAAGCTGTGACAACATGCTGATGGGCATAAAGTCTTTGAAAAAT
AGTGAAGAAGATGATGGACACACATGGCTCTTGGATGAAAGATGCTGTCTATAACTCTCCAAA
GGTGTACTTATTAATTGGATCCAGAAACAACACTGTTTGGGAATTTGCAAACATACGGGCATT
CATGGAGGATAACACCAAGCCAGCTCCCCGGAAGCAAATCCTAACACTTTCCTGGCAGGGAAC
AGGCCAAGTGATCTACAAAGGTTTTCTATTTTTTTCATAACCAAGCAACTTCTAATGAGATAAT
CAAATATAACCTGCAGAAGAGGACTGTGGAAGATCGAATGCTGCTCCCAGGAGGGGTAGGCCG
AGCATTGGTTTTACCAGCACTCCCCCTCAACTTACATTGACCTGGCTGTGGATGAGCATGGGCT
CTGGGCCATCCACTCTGGGCCAGGCACCCATAGCCATTTGGTTCTCACAAAGATTGAGCCGGG
CACACTGGGAGTGGAGCATTCTATGGGATACCCCATGCAGAAGCCAGGATGCTGAAGCCTCATT
CCTCTTGTGTGGGGTTCTCTATGTGGTCTACAGTACTGGGGGCCAGGGCCCTCATCGCATCAC
CTGCATCTATGATCCACTGGGCACTATCAGTGAGGAGGACTTGCCCAACTTGTTCTTCCCCAA
GAGACCAAGAAGTCACTCCATGATCCATTACAACCCCAAGAGATAAGCAGCTCTATGCCTGGAA
TGAAGGAAACCAGATCATTTACAACTCCAGACAAAGAGAAAGCTGCCTCTGAAG**TAA**TGCAT
TACAGCTGTGAGAAAGAGCACTGTGGCTTTGGCAGCTGTTCTACAGGACAGTGAGGCTATAGC
CCCTTCACAATATAGTATCCCTCTAATCACACAGGAAGAGTGTGTAGAAGTGGAATACGT
ATGCCTCCTTTCCCAAATGTCACCTGCCTTAGGTATCTTCCAAGAGCTTAGATGAGAGCATATC
ATCAGGAAAGTTTCAACAATGTCCATTACTCCCCCAAACCTCCTGGCTCTCAAGGATGACCAC
ATTCTGATACAGCCTACTTCAAGCCTTTTGTGTTTACTGCTCCCCAGCATTTACTGTAACTCTG
CCATCTTCCCTCCCACAATTAGAGTTGTATGCCAGCCCCTAATATTCACCACTGGCTTTTCTC
TCCCCTGGCCTTTGCTGAAGCTCTTCCCTCTTTTTTCAAATGTCTATTGATATTCTCCCATTTT
CACTGCCCCAACTAAAATACTATTAATATTTCTTTCTTTTCTTTTCTTTTTTTTGAGACAAGGT
CTCACTATGTTGCCCAGGCTGGTCTCAAACCTCCAGAGCTCAAGAGATCCTCCTGCCTCAGCCT
CCTAAGTACCTGGGATTACAGGCATGTGCCACCACACCTGGCTTAAATACTATTTCTTATTG
AGGTTTAACTCTATTTCCCTAGCCCTGTCCTTCCACTAAGCTTGGTAGATGTAATAATAAA
GTGAAAATATTAACATTTGAATATCGCTTTCAGGTGTGGAGTGTTTGCACATCATTGAATTC
TCGTTTTACCTTTGTGAAACATGCACAAGTCTTTACAGCTGTCATTCTAGAGTTTAGGTGAGT
AACACAATTACAAAGTGAAAGATACAGCTAGAAAATACTACAAATCCCATAGTTTTTCCATTG
CCCAAGGAAGCATCAAATACGTATGTTTGTTCACCTACTCTTATAGTCAATGCGTTTCATCGTT
TCAGCCTAAAATAATAGTCTGTCCCTTTAGCCAGTTTTTCATGTCTGCACAAGACCTTTCAAT
AGGCCTTTCAAATGATAATTCCTCCAGAAAACCACTAAGGGTGAGGACCCCACTCTAGCC
TCCTCTTGTCTTGCTGTCCCTCTGTTTCTCTTTCTGCTTTAAATTCAATAAAAGTGACACTG
AGCAAAAAAAAAAAAAA

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FIGURE 468

MMVALRGASALLVLFLLAAFLPPPQCTQDPAMVHYIYQRFVLEQGLEKCTQATRAYIQEFQEF
SKNISVMLGRCQTYTSEYKSAVGNLALRVERAQREIDYIQYLREADECIVSEDKTLAEMLLQE
AEEKKIRTLLNASCDNMLMGIKSLKIVKKMMDTHGSGWMKDAVYNPKVYLLIGSRNNTVWEF
ANIRAFMEDNTKPAPRKQILTLSWQGTGQVIYKGFLFFHNQATSNEIIKYNLQKRTVEDRMLL
PGGVGRALVYQHSPSTYIDLAVDEHGLWAIHSGPGTHSHLVLTKEPGTLGVEHSWDTPCRSQ
DAEASFLLCGVLYVVYSTGGQGPHRITCIYDPLGTISEEDLPNLFFPKRPRSHSMIHYNPRDK
QLYAWNEGNQIIYKLQTKRKLPLK

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FIGURE 469

TGGCCTCCCCAGCTTGCCAGGCACAAGGCTGAGCGGGAGGAAGCGAGAGGCATCTAAGCAGGC
AGTGTTTTGCCTTCACCCCCAAGTGACC**ATG**AGAGGTGCCACGCGAGTCTCAATCATGCTCCTC
CTAGTAACTGTGTCTGACTGTGCTGTGATCACAGGGGCCTGTGAGCGGGATGTCCAGTGTGGG
GCAGGCACCTGCTGTGCCATCAGCCTGTGGCTTCGAGGGCTGCGGATGTGCACCCCGCTGGGG
CGGGAAGGCGAGGAGTGCCACCCCGGCAGCCACAAGGTCCCCTTCTTCAGGAAACGCAAGCAC
CACACCTGTCTTGCTTGCCCAACCTGCTGTGCTCCAGGTTCCCGGACGGCAGGTACCGCTGC
TCCATGGACTTGAAGAACATCAATTTTT**TAG**GGCGCTTGCTTGGTCTCAGGATACCCACCATCCT
TTTCTGAGCACAGCCTGGATTTTTATTTCTGCCATGAAACCCAGCTCCCATGACTCTCCCAG
TCCCTACACTGACTACCCTGATCTCTCTTGTCTAGTACGCACATATGCACACAGGCAGACATA
CCTCCCATCATGACATGGTCCCCAGGCTGGCCTGAGGATGTCACAGCTTGAGGCTGTGGTGTG
AAAGGTGGCCAGCCTGGTTCTCTTCCCTGCTCAGGCTGCCAGAGAGGTGGTAAATGGCAGAAA
GGACATTCCCCCTCCCCTCCCAGGTGACCTGCTCTCTTTCTGGGCCCTGCCCCTCTCCCCA
CATGTATCCCTCGGTCTGAATTAGACATTCTTGGGCACAGGCTCTTGGGTGCATTGCTCAGAG
TCCCAGGTCCTGGCCTGACCCTCAGGCCCTTCACGTGAGGTCTGTGAGGACCAATTTGTGGGT
AGTTCATCTTCCCTCGATTGGTTAACTCCTTAGTTTCAGACCACAGACTCAAGATTGGCTCTT
CCCAGAGGGCAGCAGACAGTCACCCAAGGCAGGTGTAGGGAGCCCAGGGAGGCCAATCAGCC
CCCTGAAGACTCTGGTCCCAGTCAGCCTGTGGCTTGTGGCCTGTGACCTGTGACCTTCTGCCA
GAATTGTCATGCCTCTGAGGCCCCCTCTTACCACACTTTACCAGTTAACCACTGAAGCCCCCA
ATTCCCACAGCTTTTCCATTAAAATGCAAATGGTGGTGGTTCAATCTAATCTGATATTGACAT
ATTAGAAGGCAATTAGGGTGTTTCCTTAAACAACCTCCTTTCCAAGGATCAGCCCTGAGAGCAG
GTTGGTGACTTTGAGGAGGGCAGTCCTCTGTCCAGATTGGGGTGGGAGCAAGGGACAGGGAGC
AGGGCAGGGGCTGAAAGGGGCACTGATTCAGACCAGGGAGGCAACTACACACCAACATGCTGG
CTTTAGAATAAAAGCACCAACTGAAAAAA

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FIGURE 470

MRGATRVSIMLLLVTVSDCAVITGACERDVQCGAGTCCAISLWLRGLRMCTPLGREGECHPG
SHKVPFFRKRKHHTCPCLPNLLCSRFPDGRYRCSMDLKNINF

Important feratures:

Signal peptide:

amino acids 1-19

Tyrosine kinase phosphorylation site:

amino acids 88-95

N-myristoylation sites:

amino acids 33-39, 35-41, 46-52

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FIGURE 471

AGCGCCCGGGCGTCGGGGCGGTAAAAGGCCGGCAGAAGGGAGGCACTTGAGAA**ATG**TCTTTCC
TCCAGGACCCAAGTTTCTTACCATGGGGATGTGGTCCATTGGTGCAGGAGCCCTGGGGGCTG
CTGCCTTGGCATTGCTGCTTGCCAACACAGACGTGTTTCTGTCCAAGCCCCAGAAAGCGGCCC
TGGAGTACCTGGAGGATATAGACCTGAAAACACTGGAGAAGGAACCAAGGACTTTCAAAGCAA
AGGAGCTATGGGAAAAAAATGGAGCTGTGATTATGGCCGTGCGGAGGCCAGGCTGTTTCCTCT
GTCGAGAGGAAGCTGCGGATCTGTCCTCCCTGAAAAGCATGTTGGACCAGCTGGGCGTCCCCC
TCTATGCAGTGGTAAAGGAGCACATCAGGACTGAAGTGAAGGATTTCCAGCCTTATTTCAAAG
GAGAAATCTTCCTGGATGAAAAGAAAAAGTTCTATGGTCCACAAAGGCGGAAGATGATGTTTA
TGGGATTTATCCGTCTGGGAGTGTGGTACAACCTTCTTCCGAGCCTGGAACGGAGGCTTCTCTG
GAAACCTGGAAGGAGAAGGCTTCATCCTTGGGGGAGTTTTCTGTGGTGGGATCAGGAAAGCAGG
GCATTCTTCTTGAGCACCGAGAAAAAGAATTTGGAGACAAAGTAAACCTACTTTCTGTTCTGG
AAGCTGCTAAGATGATCAAACCACAGACTTTGGCCTCAGAGAAAAAA**TG**ATTGTGTGAAACTG
CCCAGCTCAGGGATAACCAGGGACATTCACCTGTGTTTCATGGGATGTATTGTTTCCACTCGTG
TCCCTAAGGAGTGAGAAACCCATTTATACTCTACTCTCAGTATGGATTATTAATGTATTTTAA
TATTCTGTTTAGGCCCACTAAGGCAAAATAGCCCCAAAACAAGACTGACAAAAATCTGAAAAA
CTAATGAGGATTATTAAGCTAAACCTGGGAAATAGGAGGCTTAAAATTGACTGCCAGGCTGG
GTGCAGTGGCTCACACCTGTAATCCCAGCACTTTGGGAGGCCAAGGTGAGCAAGTCACTTGAG
GTCGGGAGTTTCGAGACCAGCCTGAGCAACATGGCGAAACCCCGTCTCTACTAAAAATACAAAA
ATCACCCGGGTGTGGTGGCAGGCACCTGTAGTCCCAGCTACCCGGGAGGCTGAGGCAGGAGAA
TCACTTGAACCTGGGAGGTGGAGGTTGCGGTGAGCTGAGATCACACCACTGTATTCCAGCCTG
GGTGA CTGAGACTCTAACTAA

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FIGURE 472

MSFLQDPSFFTGMWWSIGAGALGAAALALLANTDVFLSKPQKALEYLEDIDLKTLEKEPRT
FKAKELWEKNGAVIMAVRRPGCFLCREEAADLSSLKSMLDQLGVPLYAVVKEHIRTEVKDFQP
YFKGEIFLDEKKKFYGPQRRKMMFMGFIRLGWYNFFRAWNGGFSGNLEGEFGFILGGVFVVG
GKQGILLEHREKEFGDKVNLLSVLEAAKMIKPQTLASEKK

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FIGURE 473

AATATATCATCTATTTATCATTAATCAATAATGTATTCTTTTATTCCAATAACATTTGGGTTT
TGGGATTTTAAATTTTCAAACACAGCAGAATGACATTTTTTCTGTCACTATTATTATTGTTGGT
ATGTGAAGCTATTTGGAGATCCAATTCAGGAAGCAACACATTGGAGAATGGCTACTTTCTATC
AAGAAATAAAGAGAACCACAGTCAACCCACACAATCATCTTTAGAAGACAGTGTGACTCCTAC
CAAAGCTGTCAAAACCACAGGCAAGGGCATAGTTAAAGGACGGAATCTTGACTCAAGAGGGTT
AATTCTTGGTGCTGAAGCCTGGGGCAGGGGTGTAAAGAAAAACACTTAGATTCAATGATTGTA
AATTTAAGGCAAATACACATATTAGTATTACCTTAGTGTAATGTATCCCTGTCATATATACAA
TAAGGTGAAATTATAAGTACCCTATGCAGTTGGCTGGACAGTTCTAAATTGGACTTTATTAAT
TTTTAAAATCAGTAACTGATTTATCACTGGCTATGTGCTTAGATCTACAGGAGATCATATAAT
TTGATACAAATAAAAGAAAAGTGTTCTCTCCCCTTACAGAATTGACATTTTAAATGCGATACA
GTTAGAATAGGAAATATGACATTAGAAAGGAAGAATGACAGGGAGAAAGGAAAGAAGGGAAAA
TGTTGCCAAGGAAAAAAAAA

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FIGURE 474

MTFFLSLLLLLVCEAIWRSNSGSNTLENGYFLSRNKENHSQPTQSSLEDSVTPTKAVKTTGKG
IVKGRNLDSRGLILGAEAWGRGVKKNT

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FIGURE 476

MAPLALHLLVLPILLSLVASQDWKAERSQDPFEKCMQDPDYEQLLKVVVTWGLNRTLKPQRVI
VVGAGVAGLVAAKVLS DAGHKVTILEADNRIGGRIFTYRDQNTGWIGELGAMRMPSSHRILHK
LCQGLGLNLTKFTQYDKNTWTEVHEVKLRNYVVEKVPEKLG YALRPQEKGHSPEDIYQMALNQ
ALKDLKALGCRKAMKKFERHTLLEYLLGEGNLSRPAVQLLGDVMS EDGFFYLSFAEALRAHSC
LSDRLQYSRIVGGWDL LPRALLSSLSGLVLLNAPVVAMTQGPHDVHVQIETSPPARNLKVLKA
DVVLLTASGPAVKRITFSPPLPRHMQEALRRLHYVPATKVFLSFRRPFWREEHIEGGHSNTDR
PSRMI FYPPPREGALLASYTWS DAAAAFAGLSREEALRLALDDVAALHGPVVRQLWDGTGVV
KRWAEDQHSQGGFVVQPPALWQTEKDDWTVPYGRIYFAGEHTAYPHGWVETAVKSALRAAIKI
NSRKGPASDTASPEGHASDMEGQGHVHGVASSPSHDLAKEEGSHPPVQGGQLSLQNTTHTRTSH

Important features:**Signal peptide:**

amino acids 1-21

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FIGURE 477

CTGACATGGCCTGACTCGGGACAGCTCAGAGCAGGGCAGAACTGGGGACACTCTGGGCCGGCCTTCTGCCTGC**AT**
GGACGCTCTGAAGCCACCTGTCTCTGGAGGAACCACGAGCGAGGGGAAGAAGGACAGGGACTCGTGTGGCAGGAA
GAACTCAGAGCCGGGAAGCCCCATTCAGTAGAAGCACTGAGAGATGCGGGCCCCCTCGCAGGGTCTGAATTTCCCT
GCTGCTGTTACAAAAGATGCTTTTTATCTTTAACTTTTTGTTTTCCCCACTTCCGACCCCGGCGTTGATCTGCAT
CCTGACATTTGGAGCTGCCATCTTCTTGTGGCTGATCACCAGACCTCAACCCGTCTTACCTCTTCTTGACCTGAA
CAATCAGTCTGTGGGAATTGAGGGAGGAGCACGGAAGGGGGTTTCCCAGAAGAACAATGACCTAACAAAGTTGCTG
CTTCTCAGATGCCAAGACTATGTATGAGGTTTTCCAAAGAGGACTCGCTGTGTCTGACAATGGGCCCTGCTTGGG
ATATAGAAAACCAAACCAGCCCTACAGATGGCTATCTTACAAACAGGTGTCTGATAGAGCAGAGTACCTGGGTTT
CTGTCTCTTGCCATAAAGGTTATAAATCATCACCAGACAGTTTGTGCGCATCTTTGCTCAGAATAGGCCAGAGTG
GATCATCTCCGAATTGGCTTGTTACACGTACTCTATGGTAGCTGTACCTCTGTATGACACCTTGGGACCAGAAGC
CATCGTACATATTGTCAACAAGGCTGATATCGCCATGGTGATCTGTGACACACCCCAAAGGCATTGGTGCTGAT
AGGGAATGTAGAGAAAAGGCTTCACCCCGAGCCTGAAGGTGATCATCCTTATGGACCCCTTTGATGATGACCTGAA
GCAAAGAGGGGAGAAGAGTGGAATTGAGATCTTATCCCTATATGATGCTGAGAACCTAGGCAAAGAGCACTTCAG
AAAACCTGTGCCTCCTAGCCCAGAAGACCTGAGCGTCATCTGCTTACCAGTGGGACCACAGGTGACCCCAAAGG
AGCCATGATAACCCATCAAAATATTGTTTCAAATGCTGCTGCCTTTCTCAAATGTGTGGAGCATGCTTATGAGCC
CACTCCTGATGATGTGGCCATATCCTACCTCCCTCTGGCTCATATGTTTGAGAGGATTGTACAGGCTGTTGTGTA
CAGCTGTGGAGCCAGAGTTGGATTCTTCCAAGGGGATATTCGGTTGCTGGCTGACGACATGAAGACTTTGAAGCC
CACATTGTTTCCCGCGGTGCCCTCGACTCCTTAACAGGATCTACGATAAGGTACAAAATGAGGCCAAGACACCCCTT
GAAGAAGTTCTTGTGAAGCTGGCTGTTTCCAGTAAATTCAAAGAGCTTCAAAGGGTATCATCAGGCATGATAG
TTTCTGGGACAAGCTCATCTTTGCAAAGATCCAGGACAGCCTGGGCGGAAGGGTTCTGTGAATTGTCACTGGAGC
TGCCCCCATGTCCACTTCAGTCATGACATTCTTCCGGGCAGCAATGGGATGTCAGGTGTATGAAGCTTATGGTCA
AACAGAATGCACAGGTGGCTGTACATTTACATTACCTGGGGACTGGACATCAGGTACGTTGGGGTGCCCTGGC
TTGCAATTACGTGAAGCTGGAAGATGTGGCTGACATGAACACTTTTACAGTGAATAATGAAGGAGAGGTCTGCAT
CAAGGGTACAAACGTGTTCAAAGGATACCTGAAGGACCCCTGAGAAGACACAGGAAGCCCTGGACAGTGATGGCTG
GCTTCACACAGGAGACATTGGTCGCTGGCTCCCGAATGGAACCTGAAGATCATCGACCGTAAAAAGAACATTTT
CAAGCTGGCCCAAGGAGAAATACATTGCACCAGAGAAGATAGAAAATATCTACAACAGGAGTCAACCAGTGTACAC
AATTTTTGTACACGGGGAGAGCTTACGGTCATCCTTAGTAGGAGTGGTGGTTTCTGACACAGATGTACTTCCCTC
ATTTGCAGCCAAGCTTGGGGTGAAGGGCTCCTTTGAGGAACTGTGCCAAAACCAAGTTGTAAGGGAAGCCATTTT
AGAAGACTTGCAGAAAATTGGGAAAGAAAGTGGCCTTAAAACCTTTTGAACAGGTCAAAGCCATTTTTCTTCATCC
AGAGCCATTTTCCATTGAAAATGGGCTCTTGACACCAACATTGAAAGCAAAGCGAGGAGAGCTTTCCAAATACTT
TCGGACCCAAATTGACAGCCTGTATGAGCACATCCAGGAT**TAG**GATAAGGTACTTAAGTACCTGCCGGCCCACTG
TGCATGCTTGTGAGAAAATGGATTAAAAACTATTCTTACATTTGTTTTGCCTTTCCTCCTATTTTTTTTTTAAACC
TGTTAAACTCTAAAGCCATAGCTTTTGTGTTTTATATTGAGACATATAATGTGTAAACTTAGTTCCCAAAATAAATCA
ATCCTGTCTTTCCCATCTTCGATGTTGCTAATATTAAGGCTTCAGGGCTACTTTTATCAACATGCCTGTCTTCAA
GATCCAGTTTATGTTCTGTGTCCTTCCTCATGATTTCCAACCTTAATACTATTAGTAACCACAAGTTCAAGGGT
CAAAGGGACCCCTCTGTGCCCTTCTTCTTTGTTTTGTGATAAAACATAAAGTCCCAACAGTCTCTATGCTTATTTACA
TCTTCTACTGTTCAAACCTAAGAGATTTTTAAATTCTGAAAACTGCTTACAATTTCATGTTTTCTAGCCACTCCAC
AAACCACTAAAATTTTAGTTTTAGCCTATCACTCATGTCAATCATATCTATGAGACAAATGTCTCCGATGCTCTT
CTGCGTAAATTAAATTGTGTAAGGGAAGTTGATCATACCAACATTTCTTAACTCTCTAGTTAGATA
TCTGACTTGGGAGTATTAATAATTGGGTCTATGACATACTGTCCAAAAGGAATGCTGTTCTTAAAGCATTATTTA
CAGTAGGAACTGGGGAGTAAATCTGTTCCCTACAGTTTGTGCTGAGCTGGAAGCTGTGGGGGAAGGAGTTGACA
GGTGGGCCCAGTGAACCTTTCCAGTAAATGAAGCAAGCACTGAATAAAAACCTCCTGAAGTGGGAACAAAGATCT
ACAGGCAAGCAAGATGCCACACACAGGCTTATTTTCTGTGAAGGAACCAACTGATCTCCCCACCCCTTGGATT
AGAGTTCCTGCTCTACCTTACCCACAGATAACACATGTTGTTTCTACTTGTAATGTAAAGTCTTTAAAAATAAAC
TATTACAGATAAAAAA

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FIGURE 478

MDALKPPCLWRNHERGKKDRDSCGRKNSEPGSPHSLEALRDAAPSQGLNLLLLFTKMLFIFNF
LFSPLPTPALICILTFGAAIFLWLITRPQPVLPLLDLNNQSVGIEGGARKGVSQKNNDLTSCC
FSDAKTMYEVFQRLAVSDNGPCLGYRKPNQPYRWLSYKQVSDRAEYLGSCLLHKGYKSSPDQ
FVGIFAQNRPEWIISELACYTYSMAVAVPLYDTLGPEAIVHIVNKADIAMVICDTPQKALVLIG
NVEKGFTP SLKVIIILMDPFDDDLKQRGEKSGIEILSLYDAENLGKEHFRKPVPPSPEDLSVIC
FTSGTTGDPKGAMITHQNIVSNAAAF LKCV E HAYEPTPDDVAISYLPLAHMFERIVQAVVYSC
GARVGFFQGDIRLLADDMKTLKPTLFPAPVPRLLNRIYDKVQNEAKTPLKKFLLKLAVSSKFKE
LQKGIIRHDSFWDKLI FAKIQDSLGRVRVIVTGAA PMSTSVM TFFRAAMGCQVYEAYGQTEC
TGGCTFTLPGDWTSGHVGVP LACNYVKLEDVADMNYFTVNNEGEVCIKGTNVFKGYLKDPEKT
QEALDSDGWLHTGDIGRWLPNGTLKIIDRKKNIFKLAQGEYIAPEKIENIYNRSQPVLQIFVH
GESLRSSLVGVVVPD TDVLP SF AAKLG VKGSFEELCQNQVVREAILEDLQKIGKESGLKTFEQ
VKAIFLHPEPF S IENGLLTPTLKA KRGE LSKYFRTQIDSLYEHIQD

Important features:**Type II transmembrane domain:**

amino acids 61-80

Putative AMP-binding domain signature.

amino acids 314-325

N-glycosylation site.

amino acids 102-105, 588-591 and 619-622

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FIGURE 479

GGAGGCGGAGGCCGCGGCGAGCCGGGCCGAGCAGTGAGGGCCCTAGCGGGGCCCCGAGCGGGGC
CCGGGGCCCCCTAAGCCATTCCTGAAGTCATGGGCTGGCCAGGACATTGGTGACCCGCCAATCC
GGT**ATG**GACGACTGGAAGCCCAGCCCCCTCATCAAGCCCTTTGGGGCTCGGAAGAAGCGGAGC
TGGTACCTTACCTGGAAGTATAAACTGACAAACCAGCGGGCCCTGCGGAGATTCTGTCAGACA
GGGGCCGTGCTTTTCTGCTGGTGACTGTCAATTGTCAATATCAAGTTGATCCTGGACACTCGG
CGAGCCATCAGTGAAGCCAATGAAGACCCAGAGCCAGAGCAAGACTATGATGAGGCCCTAGGC
CGCCTGGAGCCCCCACGGCGCAGAGGCAGTGGTCCCCGGCGGGTCCTGGACGTAGAGGTGTAT
TCAAGTCGCAGCAAAGTATATGTGGCAGTGGATGGCACCACGGTGCTGGAGGATGAGGCCCCGG
GAGCAGGGCCGGGGCATCCATGTCATTGTCTCAACCAGGCCACGGGCCACGTGATGGCAAAA
CGTGTGTTTGACACGTACTCACCTCATGAGGATGAGGCCATGGTGCTATTCTCAACATGGTA
GCGCCCCGGCCGAGTGCTCATCTGCACTGTCAAGGATGAGGGCTCCTTCCACCTCAAGGACACA
GCCAAGGCTCTGCTGAGGAGCCTGGGCAGCCAGGCTGGCCCTGCCCTGGGCTGGAGGGACACA
TGGGCCCTTCTGTGGGACGAAAAGGAGGTCTGTCTTCGGGGAGAAACATTCTAAGTCACCTGCC
CTCTCTTCTGGGGGGACCCAGTCCTGCTGAAGACAGATGTGCCATTGAGCTCAGCAGAAGAG
GCAGAGTGCCACTGGGCAGACACAGAGCTGAACCGTCGCCGCCGGCGCTTCTGCAGCAAAGTT
GAGGGCTATGGAAGTGTATGCAGCTGCAAGGACCCACACCCATCGAGTTCAGCCCTGACCCA
CTCCCAGACAACAAGGTCTCAATGTGCCTGTGGCTGTCAATTGCAGGGAACCGACCCAATTAC
CTGTACAGGATGCTGCGCTCTCTGCTTTCAGCCCAGGGGGTGTCTCCTCAGATGATAACAGTT
TTCATTGACGGCTACTATGAGGAACCCATGGATGTGGTGGCACTGTTTGGTCTGAGGGGCATC
CAGCATACTCCCATCAGCATCAAGAATGCCCGCGTGTCTCAGCACTACAAGGCCAGCCTCACT
GCCACTTTCAACCTGTTTCCGGAGGCCAAGTTTGTGTGGTTCTGGAAGAGGACCTGGACATT
GCTGTGGATTTTTTTCAGTTTCTGAGCCAATCCATCCACCTACTGGAGGAGGATGACAGCCTG
TACTGCATCTCTGCCTGGAATGACCAGGGGTATGAACACACGGCTGAGGACCCAGCACTACTG
TACCGTGTGGAGACCATGCCTGGGCTGGGCTGGGTGCTCAGGAGGTCCTTGTACAAGGAGGAG
CTTGAGCCCAAGTGGCCTACACCGGAAAAGCTCTGGGATTGGGACATGTGGATGCGGATGCCT
GAACAACGCCGGGGCCGAGAGTGCATCATCCCTGACGTTTCCCGATCCTACCACTTTGGCATC
GTCGGCCTCAACATGAATGGCTACTTTCACGAGGCCTACTTCAAGAAGCACAAAGTTCAACACG
GTTCCAGGTGTCCAGCTCAGGAATGTGGACAGTCTGAAGAAAGAAGCTTATGAAGTGGAAAGTT
CACAGGCTGCTCAGTGAGGCTGAGGTTCTGGACCACAGCAAGAACCCTTGTGAAGACTCTTTC
CTGCCAGACACAGAGGGCCACACCTACGTGGCCTTTATTTCGAATGGAGAAAGATGATGACTTC
ACCACCTGGACCCAGCTTGCCAAGTGCCTCCATATCTGGGACCTGGATGTGCGTGGCAACCAT
CGGGGCCTGTGGAGATTGTTTTCGGAAGAAGAACCCTTCTGGTGGTGGGGGTCCCGGCTTCC
CCCTACTCAGTGAAGAAGCCACCCTCAGTCACCCCAATTTTCTGGAGCCACCCCCAAAGGAG
GAGGGAGCCCCAGGAGCCCCAGAACAGACAT**TGA**GACCTCCTCCAGGACCTGCGGGGCTGGGT
ACTGTGTACCCCCAGGCTGGCTAGCCCTTCCCTCCATCCTGTAGGATTTTGTAGATGCTGGTA
GGGGCTGGGGCTACCTTGTTTTTAACATGAGACTTAATTACTAACTCCAAGGGGAGGGTTCCC
CTGCTCCAACACCCCGTTCTGAGTTAAAAGTCTATTTATTTACTTCTTGTGAGAAAGGGC
AGGAGAGTACCTGGGAATCATTACGATCCCTAGCAGCTCATCCTGCCCTTGAATACCCCTCAC
TTTCCAGGCCTGGCTCAGAATCTAACCTATTTATTGACTGTCCTGAGGGCCTTGAAAACAGGC
CGAACCTGGAGGGCCTGGATTTCTTTTTGGGCTGGAATGCTGCCCTGAGGGTGGGGCTGGCTC
TTACTCAGGAACTGCTGTGCCCAACCCATGGACAGGCCCAGCTGGGGCCCACATGCTGACAC
AGACTCACTCAGAGACCCTTAGACACTGGACCAGGCCTCCTCTCAGCCTTCTCTTTGTCCAGA
TTTCCAAAGCTGGATAAGTTGGTCATTGATTAAAAAAGGAGAAGCCCTCTGGGAAAAAAAAAA
AAAAAAAAAAAAAAAAAA

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FIGURE 480

MDDWKPSPLIKPFGARKKRSWYLTWKYKLTNQALRRFCQTGAVLFLLVTIVNIKLILDTRR
AISEANEDPEPEQDYDEALGRLEPPRRRGSGPRRVLDVEVYSSRSKVYVAVDGTTVLEDEARE
QGRGIHVIVLNQATGHVMAKRVEDTYS PHEDEAMVLFNLMVAPGRVLICTVKDEGSFHLKDTA
KALLRSLGSQAGPALGWRDTWAFVGRKGGPVFGEKHSKSPALSSWGDPVLLKTDVPLSSAEEA
ECHWADTELNRRRRRFCSKVEGYGSVCCKDPTPIEFSPDPLPDNKVLNVPVAVIAGNRPNYL
YRMLRSLLSAQGVSPQMITVFIDGYEPMDEVVALFGLRGIQHTPISIKNARVSQHYKASLTA
TFNLFPEAKFAVVLEEDLDIAVDFFSFLSQSIHLLEEDDSLYCISAWNDAQYEHTAEDPALLY
RVETMPGLGWVLRRLSYKEELEPKWPTPEKLWDWDMWMRMPEQRRGRECIIPDVSRSYHFGIV
GLNMNGYFHEAYFKKHKFNTVPGVQLRNVDLKEAYEVEVHRLLEAEVLDHKNPCEDSFL
PDTEGHTYVAFIRMEKDDDDFTTWTQLAKCLHIWDLVVRGNHRGLWRLFRKKNHFLVVGVPASP
YSVKKPPSVTPIFLEPPPKEEGAPGAPEQT

Important features:**Transmembrane domain:**

amino acids 38-55

Homologous region to Mouse GNT1

amino acids 229-660

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FIGURE 481

GAAAGAATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAACCA
GGTGCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT
GCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAAGTT
CCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGAGGGTATCA
TTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCTGTTGAGGTGCAATCA
GCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGACCAAACCTCTGGAA
TTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTGCCCATCTGGATTATT
ATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTACTGATTTTATCAGGGATC
TGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAAGTGGATGACGCTGAAGATAAGTGTGAA
AACATGATCACAATTGAAAATGGCATCCCCTCTGATCCCCTGGACATGAAGGGGGGCATATTA
ATGATGCCTTCATGACAGAGGATGAGAGGCTCACCCCTCTCTGAAGGGCTGTTGTTCTGCTTC
CTCAAGAAATTAAACATTTGTTTCTGTGTGACTGCTGAGCATCCTGAAATACCAAGAGCAGAT
CATATATTTTGTTCACCATTTCTTCTTTTGTAAATAAATTTTGAATGTGCTTGAAAGTGAAAAG
CAATCAATTATACCCACCAACACCACTGAAATCATAAGCTATTCACGACTCAAAATATTCTAA
AATATTTTTCTGACAGTATAGTGTATAAATGTGGTCATGTGGTATTTGTAGTTATTGATTTAA
GCATTTTTTAGAAATAAGATCAGGCATATGTATATATTTTCACACTTCAAAGACCTAAGGAAAA
ATAAATTTTCCAGTGGAGAATACATATAATATGGTGTAGAAATCATTGAAAATGGATCCTTTT
TGACGATCACTTATATCACTCTGTATATGACTAAGTAAACAAAAGTGAGAAGTAATTATTGTA
AATGGATGGATAAAAAATGGAATTACTCATATACAGGGTGGAAATTTTATCCTGTTATCACACCA
ACAGTTGATTATATATTTTCTGAATATCAGCCCCTAATAGGACAATTCTATTTGTTGACCATT
TCTACAATTTGTAAAAGTCCAATCTGTGCTAACTTAATAAAGTAATAATCATCTCTTTTAA
AAAAAAAAAAAAAAAAAAAAA

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FIGURE 482

MLWLLFFLVTAIHAELCQPGAENAFKVRLSIRTALGDKAYAWDTNEEYLFKAMVAFSMRKVPN
REATEISHVLLCNVTQRVSEFWFVVTDPSTKNHTLPAVEVQSAIRMNKNRINNAFFLNDQTLEFL
KIPSTLAPPMDPSVPIWIIIFGVIFCIIIVAIALLILSGIWQRRRKNKEPSEVDDAEDKCENM
ITIENGIPSDPLDMKGGILMMPS

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FIGURE 483

CGTCTCTGCGTTTCGCC**ATG**CGTCCCGGGGCGCCAGGGCCACTCTGGCCTCTGCCCTGGGGGGC
CCTGGCTTGGGGCCGTGGGCTTTCGTGAGCTCCATGGGCTCGGGGAACCCCGCGCCCGGTGGTGT
TTGCTGGCTCCAGCAGGGCCAGGAGGCCACCTGCAGCCTGGTGCTCCAGACTGATGTCACCCG
GGCCGAGTGCTGTGCCTCCGGCAACATTGACACCGCCTGGTCCAACCTCACCCACCCGGGGAA
CAAGATCAACCTCCTCGGCTTCTTGGGCCTTGTCCTACTGCCTTCCCTGCAAAGATTTCGTGCGA
CGGCGTGAGTGCGGGCCGGGCAAGGCGTGCCGCATGCTGGGGGGCGCCCGCGCTGCGAGTG
CGCGCCCGACTGCTCGGGGCTCCCGGCGCGGCTGCAGGTCTGCGGCTCAGACGGCGCCACCTA
CCGCGACGAGTGCGAGCTGCGCGCCGCGCGCTGCCGCGGCCACCCGGACCTGAGCGTCATGTA
CCGGGGCCGCTGCCGCAAGTCTGTGAGCACGTGGTGTGCCCCGCGGCCACAGTCGTGCGTTCGT
GGACCAGACGGGCAGCGCCCACTGCGTGCTGGTGTGTGAGCGGCGCCCTGCCCTGTGCCCTCCAG
CCCCGGCCAGGAGCTTTGCGGCAACAACAACGTCACCTACATCTCCTCGTGCCACATGCGCCA
GGCCACCTGCTTCTGGGCCGCTCCATCGGCGTGCGCCACGCGGGCAGCTGCGCAGGCACCCC
TGAGGAGCCGCCAGGTGGTGAGTCTGCAGAAGAGGAAGAGA**ACTT**CGT**TGA**GCCTGCAGGAC
AGGCCTGGGCTGGTGCCCCGAGGCCCCCCATCATCCCCTGTTATTTATTGCCACAGCAGAGTC
TAATTTATATGCCACGGACACTCCTTAGAGCCCGGATTTCGGACCACTTGGGGATCCCAGAACC
TCCCTGACGATATCCTGGAAGGACTGAGGAAGGGAGGCCTGGGGGCGGGCTGGTGGGTGGGAT
AGACCTGCGTTCCGGACACTGAGCGCCTGATTTAGGGCCCTTCTCTAGGATGCCCCAGCCCCCT
ACCCTAAGACCTATTGCCGGGGAGGATTCCACACTTCCGCTCCTTTGGGGATAAACCTATTAA
TTATTGCTACTATCAAGAGGGCTGGGCATTCTCTGCTGGTAATTCCTGAAGAGGCATGACTGC
TTTTCTCAGCCCCAAGCCTCTAGTCTGGGTGTGTACGGAGGGTCTAGCCTGGGTGTGTACGGA
GGGTCTAGCCTGGGTGAGTACGGAGGGTCTAGCCTGGGTGAGTACGGAGGGTCTAGCCTGGGT
GAGTACGGAGGGTCTAGCCTGGGTGTGTATGGAGGATCTAGCCTGGGTGAGTATGGAGGGTCT
AGCCTGGGTGAGTATGGAGGGTCTAGCCTGGGTGTGTATGGAGGGTCTAGCCTGGGTGAGTAT
GGAGGGTCTAGCCTGGGTGTGTATGGAGGGTCTAGCCTGGGTGAGTATGGAGGGTCTAGCCTG
GGTGTGTACGGAGGGTCTAGTCTGAGTGCGTGTGGGGACCTCAGAACACTGTGACCTTAGCCC
AGCAAGCCAGGCCCTTCATGAAGGCCAAGAAGGCTGCCACCATTCCCTGCCAGCCCAAGAACT
CCAGCTTCCCCACTGCCTCTGTGTGCCCTTTGCGTCCTGTGAAGGCCATTGAGAAATGCCCA
GTGTGCCCCCTGGGAAAGGGCACGGCCTGTGCTCCTGACACGGGCTGTGCTTGGCCACAGAAC
CACCCAGCGTCTCCCCTGCTGCTGTCCACGTCAGTTCATGAGGCAACGTCGCGTGGTCTCAGA
CGTGAGCAGCCAGCGGCAGCTCAGAGCAGGGCACTGTGTCCGGCGGAGCCAAGTCCACTCTG
GGGAGCTCTGGCGGGGACCACGGGCCACTGCTCACCCACTGGCCCCGAGGGGGGTGTAGACG
CCAAGACTCACGCATGTGTGACATCCGGAGTCCTGGAGCCGGGTGTCCAGTGGCACCCTAG
GTGCCTGCTGCCTCCACAGTGGGGTTACACCCAGGGCTCCTTGGTCCCCCACAACCTGCCCC
GGCCAGGCCTGCAGACCCAGACTCCAGCCAGACCTGCCTCACCCACCAATGCAGCCGGGGCTG
GCGACACCAGCCAGGTGCTGGTCTTGGGCCAGTTCTCCACGACGGCTCACCCCTCCCCCTCCAT
CTGCGTTGATGCTCAGAATCGCCTACCTGTGCCTGCGTGTAACCACAGCCTCAGACCAGCTA
TGGGGAGAGGACAACACGGAGGATATCCAGCTTCCCCGGTCTGGGGTGAGGAATGTGGGGAGC
TTGGGCATCCTCCTCCAGCCTCCTCCAGCCCCAGGCAGTGCCTTACCTGTGGTGCCCAGAAA
AGTGCCCCTAGGTTGGTGGGTCTACAGGAGCCTCAGCCAGGCAGCCACCCACCCCTGGGGCC
CTGCCTCACCAAGGAAATAAAGACTCAAGCCATAAAAAAA

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FIGURE 484

MRPGAPGPLWPLPWGALAWAVGVSSMSGNPAPGGVCWLQQGQEATCSLVLQTDVTRAEC
CA
SGNIDTAWSNLTHPGNKINLLGFLGLVHCLPCKDSCDGVECGPGKACRMLGGRPRCECAPDCS
GLPARLQVCGSDGATYRDECELRAARCRGHPDLSVMYRGRCRKSCHEVVCPRPQSCVVDQTGS
AHCVVCRAAPCPVPSSPGQELCGNNNVTYISSCHMRQATCFLGRSIGVRHAGSCAGTPEEPPG
GESAEEEENFV

Important features:**Signal peptide:**

amino acids 1-20

N-glycosylation sites.

amino acids 73-77, 215-219

Osteonectin domain proteins.

amino acids 97-130, 169-202

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FIGURE 485

GCTCGAGGCCGGCGGGCGGGAGAGCGACCCGGGCGGCCTCGTAGCGGGGCCCCGGATCCCC
GAGTGGCGGCCGGAGCCTCGAAAAGAGATTCTCAGCGCTGATTTTGAGATGATGGGCTTGGA
AACGGGCGTTCGCAGCATGAAGTCGCCGCCCTCGTGCTGGCCGCCCTGGTGGCCTGCATCATC
GTCTTGGGCTTCAACTACTGGATTGCGAGCTCCCGGAGCGTGGACCTCCAGACACGGATCATG
GAGCTGGAAGGCAGGGTCCGCAGGGCGGCTGCAGAGAGAGGCGCCGTGGAGCTGAAGAAGAAC
GAGTTCCAGGGAGAGCTGGAGAAGCAGCGGGAGCAGCTTGACAAAATCCAGTCCAGCCACAAC
TTCCAGCTGGAGAGCGTCAACAAGCTGTACCAGGACGAAAAGGCGGTTTTTGGTGAATAACATC
ACCACAGGTGAGAGGCTCATCCGAGTGCTGCAAGACCAGTTAAAGACCCTGCAGAGGAATTAC
GGCAGGCTGCAGCAGGATGTCCTCCAGTTTCAGAAGAACCAGACCAACCTGGAGAGGAAGTTC
TCCTACGACCTGAGCCAGTGCATCAATCAGATGAAGGAGGTGAAGGAACAGTGTGAGGAGCGA
ATAGAAGAGGTACCAAAAAGGGGAATGAAGCTGTAGCTTCCAGAGACCTGAGTGAAAACAAC
GACCAGAGACAGCAGCTCCAAGCCCTCAGTGAGCCTCAGCCCAGGCTGCAGGCAGCAGGCCTG
CCACACACAGAGGTGCCACAAGGGAAGGGAAACGTGCTTGGTAACAGCAAGTCCCAGACACCA
GCCCCCAGTTCCGAAGTGGTTTTTGGATTCAAAGAGACAAGTTGAGAAAGAGGAAACCAATGAG
ATCCAGGTGGTGAATGAGGAGCCTCAGAGGGACAGGCTGCCGCAGGAGCCAGGCCGGGAGCAG
GTGGTGGAAGACAGACCTGTAGGTGGAAGAGGCTTCGGGGGAGCCGGAGAACTGGGCCAGACC
CCACAGGTGCAGGCTGCCCTGTCAGTGAGCCAGGAAAATCCAGAGATGGAGGGGCCCTGAGCGA
GACCAGCTTGTCATCCCCGACGGACAGGAGGAGGAGCAGGAAGCTGCCGGGGAAGGGAGAAAC
CAGCAGAAACTGAGAGGAGAAGATGACTACAACATGGATGAAAATGAAGCAGAATCTGAGACA
GACAAGCAAGCAGCCCTGGCAGGGAATGACAGAAACATAGATGTTTTTAATGTTGAAGATCAG
AAAAGAGACACCATAAATTTACTTGATCAGCGTGAAAAGCGGAATCATACACTCTGAATTGAA
CTGGAATCACATATTTCAACAACAGGGCCGAAGAGATGACTATAAAATGTTTCATGAGGGACTGA
ATACTGAAAACGTGTGAAATGTACTAAATAAAATGTACATCTGA

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FIGURE 486

MMGLGNGRRSMKSPPLVLAALVACIIIVLGFNYWIIASSRSVDLQTRIMELEGRVRRAAAERGAV
ELKKNEFQGELEKQREQLDKIQSSHNFQLESVNKLYQDEKAVLVNNITTGERLIRVLQDQLKT
LQRNYGRLQQDVLQFQKNQTNLERKFSYDLSQCINQMKEVKEQCEERIEEVTKKGNEAVASRD
LSENNDQRQQQLQALSEPQPRLOAAGLPHTTEVPQGKGNVLGNSKSQTPAPSSEVVLDSKRQVEK
EETNEIQVVNEEPQRDRLPQEPGREQVVEDRVPVGGRGFGGAGELGQTPQVQAALSVSQENPEM
EGPERDQLVIPDGQEEEQEAAGEGRNQQLRGEDDYNMDENEAESETDKQAALAGNDRNIDVF
NVEDQKRDTINLLDQREKRNHTL

Important features:**Signal peptide:**

amino acids 1-29

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FIGURE 487

AACTCAAACCTCTCTCTGGGAAAACGCGGTGCTTGCTCCTCCCGGAGTGGCCTTGGCAGGG
TGTTGGAGCCCTCGGTCTGCCCCGTCCGGTCTCTGGGGCCAAGGCTGGGTTTCCCTC**ATG**TAT
GGCAAGAGCTCTACTCGTGCGGTGCTTCTTCTCCTTGGCATAACAGCTCACAGCTCTTTGGCCT
ATAGCAGCTGTGGAAATTTATACCTCCCGGGTGCTGGAGGCTGTTAATGGGACAGATGCTCGG
TTAAAATGCACTTTCTCCAGCTTTGCCCCTGTGGGTGATGCTCTAACAGTGACCTGGAATTTT
CGTCCTCTAGACGGGGGACCTGAGCAGTTTGTATTCTACTACACATAGATCCCTTCCAACCC
ATGAGTGGGCGGTTTAAGGACCGGGTGTCTTGGGATGGGAATCCTGAGCGGTACGATGCCTCC
ATCCTTCTCTGGAAACTGCAGTTCGACGACAATGGGACATACACCTGCCAGGTGAAGAACCCA
CCTGATGTTGATGGGGTGATAGGGGAGATCCGGCTCAGCGTCGTGCACACTGTACGCTTCTCT
GAGATCCACTTCCTGGCTCTGGCCATTGGCTCTGCCTGTGCACTGATGATCATAATAGTAATT
GTAGTGGTCCTCTTCCAGCATTACCGGAAAAAGCGATGGGCCGAAAGAGCTCATAAAGTGGTG
GAGATAAAATCAAAAGAAGAGGAAAGGCTCAACCAAGAGAAAAAGGTCTCTGTTTATTTAGAA
GACACAGAC**TAA**CAATTTTAGATGGAAGCTGAGATGATTTCCAAGAACAAGAACCCTAGTATT
TCTTGAAGTTAATGGAACTTTTCTTTGGCTTTTCCAGTTGTGACCCGTTTTCCAACCAGTTC
TGCAGCATATTAGATTCTAGACAAGCAACACCCCTCTGGAGCCAGCACAGTGCTCCTCCATAT
CACCAGTCATACACAGCCTCATTATTAAGGTCTTATTTAATTTTCAGAGTGTAATTTTTTCAA
GTGCTCATTAGGTTTTATAACAAGAAGCTACATTTTTGCCCCTAAGACACTACTTACAGTGT
TATGACTTGTATACACATATATTGGTATCAAAGGGGATAAAAGCCAATTTGTCTGTACATTT
CCTTTCACGTATTTCTTTTAGCAGCACTTCTGCTACTAAAGTTAATGTGTTTACTCTCTTTCC
TTCCCACATTCTCAATTAAAAGGTGAGCTAAGCCTCCTCGGTGTTTCTGATTAACAGTAAATC
CTAAATTCAAACGTGTTAAATGACATTTTTATTTTTATGTCTCTCCTTAACATGAGACACATC
TTGTTTTACTGAATTTCTTTCAATATTCCAGGTGATAGATTTTTTGTCG

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FIGURE 488

MYGKSSTRAVLLLLGIQLTALWPAAVEIYTSRVLEAVNGTDARLKCTFSSFAPVGDALTVTW
NFRPLDGGPEQFVFYYHIDPFQPMSEGRFKDRVSWDGNPERYDASILLWKLQFDDNGTYTCQVK
NPPDVDGVIGEIRLSVVHTVRFSEIHFLALAIQSACALMIIIVIVVVLQHYRKKRWAERAHK
VVEIKSKEEERLNQEKVSVYLEDTD

FIGURE 489

[illegible]

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FIGURE 490

MLLLWVSVVAALALAVLAPGAGEQRRRAAKAPNVVLVVSDFSFDGRLTFHPGSQVVKLPFINFM
KTRGTSFLNAYTNSPICCPSRAAMWSGLEFTHLTESWNNFKGLDPNYTTWMDVMERHGYRTQKF
GKLDYTS GHHSISNRVEAWTRDVAFLLRQEGRPMVNLIRNRTKVRVMERDWQNTDKAVNWLRLK
EAINYTEPFVIYLG LNLPHYPSPSSGENFGSSTFHTSLYWLEKVSHDAIKIPKWSPLSEMHP
VDYYSSYTKNCTGRFTKKEIKNIRAFYYAMCAETDAMLGEIILALHQLDLLQKTIVIIYSSDHG
ELAMEHRQFYKMSMYEASAHVPLLMMGPGIKAGLQVSNVSLVDIYPTMLDIAGIPLPQNLSG
YSLPLSSETFKNEHKVKNLHPPWILSEFHGCNVNASTYMLRTNHWKYIAYSDGASILPQLFD
LSSDPDELTNVAVKFPEITYSLDQKLHSIINYPKVSASVHQYNKEQFIKWKQSIGQNYSNVIA
NLRWHQDWQKEPRKYENAIQWLKTHMNPRAV

Important features:**Signal peptide:**

amino acids 1-15

N-glycosylation sites.amino acids 108-111, 166-169, 193-196, 262-265, 375-378, 413-416,
498-501**Sulfatases proteins:**

amino acids 286-315, 359-369, 78-97

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FIGURE 491

GAGAGAAGTCAGCCTGGCAGAGAGACTCTGAAATGAGGGATTAGAGGTGTTCAAGGAGCAAGA
GCTTCAGCCTGAAGACAAGGGAGCAGTCCCTGAAGACGCTTCTACTGAGAGGTCTGCC**ATGGC**
CTCTCTTGGCCTCCAACCTTGTGGGCTACATCCTAGGCCTTCTGGGGCTTTTGGGCACACTGGT
TGCCATGCTGCTCCCCAGCTGGAAAACAAGTTCTTATGTCGGTGCCAGCATTGTGACAGCAGT
TGGCTTCTCCAAGGGCCTCTGGATGGAATGTGCCACACACAGCACAGGCATCACCCAGTGTGA
CATCTATAGCACCCCTTCTGGGCCTGCCCCTGACATCCAGGCTGCCCAGGCCATGATGGTGAC
ATCCAGTGCAATCTCCTCCCTGGCCTGCATTATCTCTGTGGTGGGCATGAGATGCACAGTCTT
CTGCCAGGAATCCCGAGCCAAAGACAGAGTGGCGGTAGCAGGTGGAGTCTTTTTCATCCTTGG
AGGCCTCCTGGGATTTCATTCCTGTTGCCTGGAATCTTCATGGGATCCTACGGGACTTCTACTC
ACCACTGGTGCCTGACAGCATGAAATTTGAGATTGGAGAGGCTCTTTACTTGGGCATTATTTTC
TTCCCTGTTCTCCCTGATAGCTGGAATCATCCTCTGCTTTTCCTGCTCATCCCAGAGAAATCG
CTCCAATACTACGATGCCTACCAAGCCCAACCTCTTGCCACAAGGAGCTCTCCAAGGCCTGG
TCAACCTCCCAAAGTCAAGAGTGAGTTCAATTCCTACAGCCTGACAGGGTATGTG**TGA**AGAAC
CAGGGGCCAGAGCTGGGGGGTGGCTGGGTCTGTGAAAAACAGTGGACAGCACCCCGAGGGCCA
CAGGTGAGGGACACTACCACTGGATCGTGTGAGAAGGTGCTGCTGAGGATAGACTGACTTTGG
CCATTGGATTGAGCAAAGGCAGAAATGGGGGCTAGTGTAACAGCATGCAGGTTGAATTGCCAA
GGATGCTCGCCATGCCAGCCTTTCTGTTTTCTCTCACCTTGCTGCTCCCCTGCCCTAAGTCCCC
AACCTCAACTTGAAACCCCATTCCTTAAGCCAGGACTCAGAGGATCCCTTTGCCCTCTGGT
TTACCTGGGACTCCATCCCCAAACCCACTAATCACATCCCACTGACTGACCCTCTGTGATCAA
AGACCTCTCTCTGGCTGAGGTTGGCTCTTAGCTCATTGCTGGGGATGGGAAGGAGAAGCAGT
GGCTTTTGTGGGCATTGCTCTAACCTACTTCTCAAGCTTCCCTCCAAAGAACTGATTGGCCC
TGGAACCTCCATCCCACTCTTGTTATGACTCCACAGTGTCCAGACTAATTTGTGCATGAACTG
AAATAAAACCATCCTACGGTATCCAGGGAACAGAAAGCAGGATGCAGGATGGGAGGACAGGAA
GGCAGCCTGGGACATTTAAAAAATA

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FIGURE 492

MASLGLQLVG YILGLLGLLGTLVAMLLPSWKTSSYVGASIVTAVGFSKGLWMECATHSTGITQ
CDIYSTLLGLPADIQAAQAMMVTSSAIISSLACIIISVVGMRCTVFCQESRAKDRVAVAGGVFFI
LGLLGFIPVAWNLHGILRDFYSPLVPDSMKFEIGEALYLGIISSLFSLIAGIILCFSCSSQR
NRSNYYDAYQAQPLATRSSPRPGQPPKVKSEFNYSYSLTGYV

Important features:**Signal peptide:**

amino acids 1-24

Transmembrane domains:

amino acids 82-102, 117-140, 163-182

N-glycosylation site.

amino acids 190-193

PMP-22 / EMP / MP20 family proteins.

amino acids 46-59

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FIGURE 493

GCACTGCTGCTGTCCCATCAGCTGCTCTGAAGCTCCATGGTGCCCAGAATCTTCGCTCCTGCT
TATGTGTCAGTCTGTCTCCTCCTCTTGTGTCCAAGGGAAGTCATCGCTCCCGCTGGCTCAGAA
CCATGGCTGTGCCAGCCGGCACCCAGGTGTGGAGACAAGATCTACAACCCCTTGGAGCAGTGC
TGTTACAATGACGCCATCGTGTCCCTGAGCGAGACCCGCCAATGTGGTCCCCCCTGCACCTTC
TGGCCCTGCTTTGAGCTCTGCTGTCTTGATTCTTTGGCCTCACAAACGATTTTGTTGTGAAG
CTGAAGGTTTCAGGGTGTGAATTCCCAGTGCCACTCATCTCCCATCTCCAGTAAATGTGAAAGC
AGAAGACGTTTTCCCTGAGAAGACATAGAAAGAAAATCAACTTTCACTAAGGCATCTCAGAAA
CATAGGCTAAGGTAATATGTGTACCAGTAGAGAAGCCTGAGGAATTTACAAAATGATGCAGCT
CCAAGCCATTGTATGGCCCATGTGGGAGACTGATGGGACATGGAGAATGACAGTAGATTATCA
GGAAATAAATAAAGTGGTTTTTCCAATGTACACACCTGTAAAA

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FIGURE 494

MVPRI FAPAYVSVCLLLCPREVIAPAGSEPWLCQPAPRCGDKIYNPLEQCCYNDAIVSLSET
RQCGPPCTFWPCFELCCLDSFGLTNDVFVVKLVQGVNSQCHSSPISSKCESRRRFP

Important features:

Signal peptide:

amino acids 1-25

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FIGURE 495

CTCCACTGCAACCACCCAGAGCC**ATG**GCTCCCCGAGGCTGCATCGTAGCTGTCTTTGCCATTT
TCTGCATCTCCAGGCTCCTCTGCTCACACGGAGCCCCAGTGGCCCCCATGACTCCTTACCTGA
TGCTGTGCCAGCCACACAAGAGATGTGGGGACAAGTTCTACGACCCCCTGCAGCACTGTTGCT
ATGATGATGCCGTCGTGCCCTTGGCCAGGACCCAGACGTGTGGAAACTGCACCTTCAGAGTCT
GCTTTGAGCAGTGCTGCCCCCTGGACCTTCATGGTGAAGCTGATAAACCAGAACTGCGACTCAG
CCCGGACCTCGGATGACAGGCTTTGTGCGAGTGTGAGC**TAA**TGGAACATCAGGGGAACGATGA
CTCCTGGATTCTCCTTCCTGGGTGGGCCTGGAGAAAGAGGCTGGTGTACCTGAGATCTGGGA
TGCTGAGTGGCTGTTTGGGGGCCAGAGAAACACACACTCAACTGCCCCACTTCATTCTGTGACC
TGTCTGAGGCCCCACCCTGCAGCTGCCCTGAGGAGGCCCCACAGGTCCCCTTCTAGAATTCTGGA
CAGCATGAGATGCGTGTGCTGATGGGGGCCAGGGACTCTGAACCCTCCTGATGACCCCTATG
GCCAACATCAACCCGGCACCAACCCCAAGGCTGGCTGGGGAACCCTTCACCCTTCTGTGAGATT
TTCCATCATCTCAAGTTCTCTTCTATCCAGGAGCAAAGCACAGGATCATAATAAATTTATGTA
CTTTATAAATGAAAA

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FIGURE 496

MAPRGCIVAVFAIFCISRLLC SHGAPVAPMTPYLMLCQPHKRCGDKFYDPLQHCCYDDAVVPL
ARTQTCGNCTFRVCFEQCCPWTFMVKLINQNCDSARTSDDRLCRSVS

Important features:

Signal peptide:

amino acids 1-24

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FIGURE 497

TGAAGGACTTTTCCAGGACCCAAGGCCACACACTGGAAGTCTTGCAGCTGAAGGGAGGCACTC
CTTGGCCTCCGCAGCCGATCAC**ATGA**AGGTGGTGCCAAGTCTCCTGCTCTCCGTCCTCCTGGC
ACAGGTGTGGCTGGTACCCGGCTTGGCCCCCAGTCCTCAGTCGCCAGAGACCCAGCCCCTCA
GAACCAGACCAGCAGGGTAGTGCAGGCTCCCAGGGAGGAAGAGGAAGATGAGCAGGAGGCCAG
CGAGGAGAAGGCCGGTGAGGAAGAGAAAGCCTGGCTGATGGCCAGCAGGCAGCAGCTTGCCAA
GGAGACTTCAAACCTTCGGATTACGCCTGCTGCGAAAGATCTCCATGAGGCACGATGGCAACAT
GGTCTTCTCTCCATTTGGCATGTCCTTGGCCATGACAGGCTTGATGCTGGGGGCCACAGGGCC
GACTGAAACCCAGATCAAGAGAGGGCTCCACTTGCAGGCCCTGAAGCCCACCAAGCCCCGGGCT
CCTGCCTTCCCTCTTTAAGGGACTCAGAGAGACCCTCTCCCGCAACCTGGAAGTGGGCCTCTC
ACAGGGGAGTTTTGCCTTCATCCACAAGGATTTTGATGTCAAAGAGACTTTCTTCAATTTATC
CAAGAGGTATTTTGATACAGAGTGCGTGCCTATGAATTTTCGCAATGCCTCACAGGCCAAAAG
GCTCATGAATCATTACATTAACAAAGAGACTCGGGGGAAAATTTCCCAAACGTGTTTGATGAGAT
TAATCCTGAAACCAAATTAATTCTTGTGGATTACATCTTGTTCAAAGGGAAATGGTTGACCCC
ATTTGACCCTGTCTTCACCGAAGTCGACACTTTCCACCTGGACAAGTACAAGACCATTAAGGT
GCCCATGATGTACGGTGCAGGCAAGTTTGCCTCCACCTTTGACAAGAATTTTCGTTGTCTATGT
CCTCAAACGTGCCCTACCAAGGAAATGCCACCATGCTGGTGGTCCCTCATGGAGAAAATGGGTGA
CCACCTCGCCCTTGAAGACTACCTGACCACAGACTTGGTGGAGACATGGCTCAGAAACATGAA
AACCAGAAACATGGAAGTTTTCTTTCCGAAGTTCAAGCTAGATCAGAAGTATGAGATGCATGA
GCTGCTTAGGCAGATGGGAATCAGAAGAATCTTCTCACCCCTTTGCTGACCTTAGTGAACCTCTC
AGCTACTGGAAGAAATCTCCAAGTATCCAGGGTTTTACGAAGAACAGTGATTGAAGTTGATGA
AAGGGGCACTGAGGCAGTGGCAGGAATCTTGTCAGAAATTACTGCTTATTCCATGCCTCCTGT
CATCAAAGTGGACCGGCCATTTCAATTCATGATCTATGAAGAAACCTCTGGAATGCTTCTGTT
TCTGGGCAGGGTGGTGAATCCGACTCTCCTA**TAA**TTCAGGACATGCATAAGCACTTCGTGCTG
TAGTAGATGCTGAATCTGAGGTATCAAACACACACAGGATACCAGCAATGGATGGCAGGGGAG
AGTGTTCCTTTTGTTCTTAACTAGTTTAGGGTGTTCTCAAATAAATACAGTAGTCCCCACTTA
TCTGAGGGGGATACATTCAAAGACCCCCAGCAGATGCCTGAAACGGTGGACAGTGCTGAACCT
TATATATATTTTTTCTACACATACATACCTATGATAAAGTTTAATTTATAAATTAGGCACAG
TAAGAGATTAAACAATAATAACAACATTAAAGTAAAATGAGTTACTTGAACGCAAGCACTGCAAT
ACCATAACAGTCAAACCTGATTATAGAGAAGGCTACTAAGTGACTCATGGGCGAGGAGCATAGA
CAGTGTGGAGACATTGGGCAAGGGGAGAATTACATCCTGGGTGGGACAGAGCAGGACGATGC
AAGATTCCATCCCCTACTCAGAAATGGCATGCTGCTTAAGACTTTTAGATTGTTTATTTCTGG
AATTTTTTCATTTAATGTTTTTGGACCATGGTTGACCATGGTTAACTGAGACTGCAGAAAGCAA
AACCATGGATAAGGGAGGACTACTACAAAAGCATTAATTTGATACATATTTTTTAAAAAAA
AAAAAAA

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FIGURE 498

MKVVPSLLLSVLLAQVWLVPGLAPSPQSPETPAPQNQTSRVVQAPREEEDEQEASEEEKAGEE
EKAWLMASRQQLAKETSNFGFSLLRKISMRHDGNMVFSFPGMSLAMTGLMLGATGPTETQIKR
GLHLQALKPTKPGLLPSLFKGLRETLNRNLELGLSQGSFAFIHKDFDVKETFFNLSKRYFDTE
CVPMNFRNASQAKRLMNHYINKETRGKIPKLFDEINPETKLILVDYILFKGKWLTDFDPVFTE
VDTFHLDKYKTIKVPMMYGAGKFASTFDKNFRCHVLKLPYQGNATMLVVLMEKMGDHLALEDY
LTTDLVETWLRNMKTRNMEVFFPKFKLDQKYEMHELLRQMGIRRIFFSPFADLSELSATGRNLQ
VSRVLRRTVIEVDERGTEAVAGILSEITAYSMPPVIKVDRPFHFMIYEETSGMLLFLGRVVNP
TLL

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FIGURE 499

[illegible]

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FIGURE 500

MDSLRLKMLISVAMLGAGAGVGYALLVIVTPGERRKQEMLKEMPLQDPRSREEAARTQQLLLAT
LQEAATTQENVAWRKNWMVGGEGGASGRSP

Important features:

Signal peptide:

amino acids 1-18

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FIGURE 501

[illegible]

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FIGURE 502

MGPSTPLLILFLLSWGPLQGQQHHLVEYMERRLAALAEERLAQCQDQSSRHAAELRDFKNKML
PLLEVAEKEREALRTEADTISGRVDRLEREVDYLETQNPALPCVEFDEKVTGGPGTKGKGRRN
EKYDMVTDCGYTISQVRSMKILKRFGGPAGLWTKDPLGQTEKIYVLDGTQNDTAFVFPRLRDF
TLAMAARKASRVRVFPWPVGTGQLVYGGFLYFARRPPGRPGGGEMENTLQLIKFHLANRTVV
DSSVFPAEGLIPPYGLTADTYIDLVADEEGLWAVYATREDDRHLCLAKLDPQTLDTQQWDTP
CPRENAEAAAFVICGTLYVVYNTRPASRARIQCSFDASGTLTPERAALPYFPRRYGAHASLRYN
PRERQLYAWDDGYQIVYKLEMRKKEEV

Important features:**Signal peptide:**

amino acids 1-21

N-glycosylation sites.

amino acids 177-180, 248-251

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FIGURE 503

TGCGGCGCAGTGTAGACCTGGGAGGATGGGCGGCCTGCTGCTGGCTGCTTTTCTGGCTTTGGT
CTCGGTGCCCAGGGCCCAGGCCGTGTGGTTGGGAAGACTGGACCCTGAGCAGCTTCTTGGGCC
CTGGTACGTGCTTGCGGTGGCCTCCCGGGAAAAGGGCTTTGCCATGGAGAAGGACATGAAGAA
CGTCGTGGGGGTGGTGGTGACCCTCACTCCAGAAAACAACCTGCGGACGCTGTCCTCTCAGCA
CGGGCTGGGAGGGTGTGACCAGAGTGTGATGGACCTGATAAAGCGAAACTCCGGATGGGTGTT
TGAGAATCCCTCAATAGGCGTGCTGGAGCTCTGGGTGCTGGCCACCAACTTCAGAGACTATGC
CATCATCTTCACTCAGCTGGAGTTCGGGGACGAGCCCTTCAACACCGTGGAGCTGTACAGTCT
GACGGAGACAGCCAGCCAGGAGGCCATGGGGCTCTTCACCAAGTGGAGCAGGAGCCTGGGCTT
CCTGTCACAGTAGCAGGCCCAGCTGCAGAAGGACCTCACCTGTGCTCACAAGATCCTTCTGTG
AGTGCTGCGTCCCCAGTAGGGATGGCGCCACAGGGTCCTGTGACCTCGGCCAGTGTCCACCC
ACCTCGCTCAGCGGCTCCCGGGGCCAGCACCAGCTCAGAATAAAGCGATTCCACAGCA

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FIGURE 504

MGGLLLAFLALVSVPRQAQAVWLGRLDPEQLLGPWYVLAVASREKGFAMEKDMKNVVGVVVTL
TPENNLRTLSSQHGLGGCDQSVMDLIKRN'SGWVFENPSIGVLELWVLATNFRDYAIIFTQLEF
GDEPFNTVELYSLTETASQEAMGLFTKWSRSLGFLSQ

Important features:

Signal peptide:

amino acids 1-20

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FIGURE 505

GTTCCGCAGATGCAGAGGTTGAGGTGGCTGCGGGACTGGAAGTCATCGGGCAGAGGTCTCACA
GCAGCCAAGGAACCTGGGGCCCGCTCCTCCCCCCTCCAGGCC**ATG**AGGATTCTGCAGTTAATC
CTGCTTGCTCTGGCAACAGGGCTTGTAGGGGGAGAGACCAGGATCATCAAGGGGTTTCGAGTGC
AAGCCTCACTCCCAGCCCTGGCAGGCAGCCCTGTTTCGAGAAGACGCGGCTACTCTGTGGGGCG
ACGCTCATCGCCCCCAGATGGCTCCTGACAGCAGCCCACTGCCTCAAGCCCCGCTACATAGTT
CACCTGGGGCAGCACAACTCCAGAAGGAGGAGGGCTGTGAGCAGACCCGGACAGCCACTGAG
TCCTTCCCCCACCCGGCTTCAACAACAGCCTCCCCAACAAAGACCACCGCAATGACATCATG
CTGGTGAAGATGGCATCGCCAGTCTCCATCACCTGGGCTGTGCGACCCCTCACCTCTCCTCA
CGCTGTGTCACTGCTGGCACCAGCTGCCTCATTTCCGGCTGGGGCAGCACGTCCAGCCCCCAG
TTACGCCTGCCTCACACCTTGCGATGCGCCAACATCACCATCATTGAGCACCAGAAGTGTGAG
AACGCCTACCCCGGCAACATCACAGACACCATGGTGTGTGCCAGCGTGCAGGAAGGGGGCAAG
GACTCCTGCCAGGGTGACTCCGGGGGGCCCTCTGGTCTGTAACCAGTCTCTTCAAGGCATTATC
TCCTGGGGCCAGGATCCGTGTGCGATCACCCGAAAGCCTGGTGTCTACACGAAAGTCTGCAAA
TATGTGGA CTGGATCCAGGAGACGATGAAGAACAAT**TAG**ACTGGACCCACCCACCACAGCCCA
TCACCCTCCATTTCCACTTGGTGTGTTGGTTCCTGTTCACTCTGTTAATAAGAAACCCTAAGCC
AAGACCCTCTACGAACATTCTTTGGGCCTCCTGGACTACAGGAGATGCTGTCACTTAATAATC
AACCTGGGGTTCGAAATCAGTGAGACCTGGATTCAAATTCTGCCTTGAAATATTGTGACTCTG
GGAATGACAACACCTGGTTTGTCTCTGTTGTATCCCCAGCCCCAAAGACAGCTCCTGGCCAT
ATATCAAGGTTTCAATAAATATTTGCTAAATGAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
AAAAAA

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FIGURE 506

MRILQLILLALATGLVGGETRIIKGFECKPHSQPWQAALFEKTRLLCGATLIAPRWLLTAAHC
LKPRYIVHLGQHNQLQKEEGCEQTRTATESFPHPGFNNSLPNKDHRNDIMLVKMASPVSITWAV
RPLTLSSRCVTAGTSC LISGWGSTSSPQLRLPHTLRCANITII EHQKCENAYPGNITDTMVCA
SVQEGGKDSCQGD SGGPLVCNQSLQGIISWGQDPCAITRKPGVYTKVCKYVDWIQETMKNN

Important features:**Signal peptide:**

amino acids 1-18

Serine proteases, trypsin family, histidine active site.

amino acids 58-63

N-glycosylation sites.

amino acids 99-102, 165-168, 181-184, 210-213

Glycosaminoglycan attachment site.

amino acids 145-148

Kringle domain proteins.

amino acids 197-209, 47-64

Serine proteases, trypsin family, histidine protein

amino acids 199-209, 47-63, 220-243

Apple domain proteins

amino acids 222-249, 189-222

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FIGURE 507

CTGGGATCAGCCACTGCAGCTCCCTGAGCACTCTCTACAGAGACGCGGACCCCAGAC**ATG**AGG
AGGCTCCTCCTGGTCACCAGCCTGGTGGTTGTGCTGCTGTGGGAGGCAGGTGCAGTCCCAGCA
CCCAAGGTCCCTATCAAGATGCAAGTCAAACACTGGCCCTCAGAGCAGGACCCAGAGAAGGCC
TGGGGCGCCCGTGTGGTGGAGCCTCCGGAGAAGGACGACCAGCTGGTGGTGCTGTTCCCTGTC
CAGAAGCCGAAACTCTTGACCACCGAGGAGAAGCCACGAGGTCAGGGCAGGGGGCCCCATCCTT
CCAGGCACCAAGGCCTGGATGGAGACCGAGGACACCCTGGGCCGTGTCCTGAGTCCCGAGCCC
GACCATGACAGCCTGTACCACCCTCCGCCTGAGGAGGACCAGGGCGAGGAGAGGCCCCGGTTG
TGGGTGATGCCAAATCACCAGGTGCTCCTGGGACCGGAGGAAGACCAAGACCACATCTACCAC
CCCCAG**TAG**GGCTCCAGGGGCCATCACTGCCCCCGCCCTGTCCCAAGGCCCAGGCTGTTGGGA
CTGGGACCCTCCCTACCCTGCCCCAGCTAGACAAATAAACCCCAGCAGGCAAAAAAAAAAAAAA
AAAAAA

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FIGURE 508

MRRLLLVTSLVVLLWEAGAVPAPKVPIKMQVKHWPSEQDPEKAWGARVVEPPEKDDQLVVLF
PVQKPKLLTTEEKPRGQGGRGPILPGTKAWMETEDTLGRVLSPEPDHDSLYHPPPEEDQGEERP
RLWVMPNHQVLLGPEEDQDHIYHPQ

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FIGURE 509

GCGGAGCCGGCGCCGGCTGCGCAGAGGAGCCGCTCTCGCCGCCGCCACCTCGGCTGGGAGCCC
ACGAGGCTGCCGCATCCTGCCCTCGGAACAATGGGACTCGGCGCGCGAGGTGCTTGGGCGCG
CTGCTCCTGGGGACGCTGCAGGTGCTAGCGCTGCTGGGGGCCGCCATGAAAGCGCAGCCATG
GCGGCATCTGCAAACATAGAGAATTCTGGGCTTCCACACAACCTCCAGTGCTAACTCAACAGAG
ACTCTCCAACATGTGCCTTCTGACCATACAAATGAACTTCCAACAGTACTGTGAAACCACCA
ACTTCAGTTGCCTCAGACTCCAGTAATACAACGGTCACCACCATGAAACCTACAGCGGCATCT
AATACAACAACACCAGGGATGGTCTCAACAAATATGACTTCTACCACCTTAAAGTCTACACCC
AAAACAACAAGTGTTTCACAGAACACATCTCAGATATCAACATCCACAATGACCGTAACCCAC
AATAGTTCAGTGACATCTGCTGCTTCATCAGTAACAATCACAACAACCTATGCATTCTGAAGCA
AAGAAAGGATCAAAATTTGATACTGGGAGCTTTGTTGGTGGTATTGTATTAACGCTGGGAGTT
TTATCTATTCTTTACATTGGATGCAAAATGTATTACTCAAGAAGAGGCATTCGGTATCGAACC
ATAGATGAACATGATGCCATCATTTAAGGAAATCCATGGACCAAGGATGGAATACAGATTGAT
GCTGCCCTATCAATTAATTTTGGTTTATTAATAGTTTAAAACAATATTCTCTTTTTTGAAAATA
GTATAAACAGGCCATGCATATAATGTACAGTGTATTACGTAAATATGTAAAGATTCTTCAAGG
TAACAAGGGTTTGGGTTTTGAAATAAACATCTGGATCTTATAGACCGTTCATACAATGGTTTT
AGCAAGTTCATAGTAAGACAAACAAGTCCTATCTTTTTTTTTTTGGCTGGGGTGGGGGCATTGG
TCACATATGACCAGTAATTGAAAGACGTCATCACTGAAAGACAGAATGCCATCTGGGCATACA
AATAAGAAGTTTGTACAGCACTCAGGATTTTGGGTATCTTTTGTAGCTCACATAAAGAACTT
CAGTGCTTTTCAGAGCTGGATATATCTTAATTACTAATGCCACACAGAAATTATACAATCAAA
CTAGATCTGAAGCATAATTTAAGAAAAACATCAACATTTTTTGTGCTTTAACTGTAGTAGTT
GGTCTAGAAACAAAATACTCC

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FIGURE 510

MGLGARGAWAALLLGTLQVLALLGAAHESAAMAASANIENSGLPHNSSANSTETLQHVPDHT
NETSNSTVKPPTSVASDSSNTTVTTMKPTAASNTTTPGMVSTNMTSTTLKSTPKTTSVSQNTS
QISTSTMTVTHNSSVTSAASSVTITTTMHSEAKKGSKFDTGSFVGGIVLTLGVLSILYIGCKM
YYSRRGIRYRTIDEHDAII

FIGURE 511

GACTTTGCTTGAATGTTTACATTTTCTGCTCGCTGCTCTACATATCACAAATATAGTGTTCACGTTTTGTTAAAAAC
TTTGGGGTGT CAGGAGTTGAGCTTGCTCAGCAAGCCAGCATGGCTAGGATGAGCTTTGTTATAGCAGCTTGCCAA
TTGGTGCTGGGCCTACTAATGACTTCATTAACCGAGTCTTCCATACAGAATAGTGAGTGTCCACAACCTTTGCGTA
TGTGAAATTCGTCCCTGGTTTTACCCACAGTCAACTTACAGAGAAGCCACCAGTGTGATTGCAATGACCTCCGC
TTAACAAGGATTCCCAGTAACCTCTCTAGTGACACACAAGTGCTTCTCTTACAGAGCAATAACATCGCGAAGACT
GTGGATGAGCTGCAGCAGCTTTTCAACTTGACTGAACTAGATTTCTCCCAAACAACCTTTACTAACATTAAGGAG
GTCGGGCTGGCAAACCTAACCCAGCTCACAAACGCTGCATTTGGAGGAAAATCAGATTACCGAGATGACTGATTAC
TGTCTACAAGACCTCAGCAACCTTCAAGAACTCTACATCAACCACAACCAAATTAGCACTATTTCTGCTCATGCT
TTTGCAGGCTTAAAAAATCTATTAAGGCTCCACCTGAACTCCAACAAATTGAAAGTTATTGATAGTCGCTGGTTT
GATTCTACACCCAACCTGGAAATTCTCATGATCGGAGAAAACCTGTGATTGGAATTCTGGATATGAACTTCAA
CCCCCTCGCAAATTTGAGAAGCTTAGTTTTTGGCAGGAATGTATCTCACTGATATTCCTGGAAATGCTTTGGTGGGT
CTGGATAGCCTTGAGAGCCTGTCTTTTTATGATAACAACTGGTTAAAGTCCCTCAACTTGCCCTGCAAAAAGTT
CCAAATTTGAAATTCTTAGACCTCAACAAAAACCCCATTCACAAAATCCAAGAAGGGGACTTCAAAAATATGCTT
CGGTTAAAGAAGCTGGGAATCAACAATATGGGCGAGCTCGTTTTCTGTGCGACCGCTATGCCCTGGATAACTTGCCT
GAACTCACAAAGCTGGAAGCCACCAATAACCCCTAACTCTCTTACATCCACCGCTTGGCTTTCGGAAGTGTCCT
GCTCTGGAAAGCTTGATGCTGAACAACAATGCCTTGAATGCCATTTACCAAAGACAGTCGAATCCCTCCCCAAT
CTGCGTGAGATCAGTATCCATAGCAATCCCCCTCAGGTGTGACTGTGTGATCCACTGGATTAACTCCAACAAAACC
AACATCCGCTTCATGGAGCCCCTGTCCATGTTCTGTGCCATGCCGCCGAATATAAAGGGCACCAGGTGAAGGAA
GTTTTAATCCAGGATTTCGAGTGAACAGTGCCTCCCAATGATATCTCACGACAGCTTCCCAAATCGTTTTAAACGTG
GATATCGGCACGACGTTTTTCTAGACTGTGAGCCATGGCTGAGCCAGAACCTGAAATTTACTGGGTCACTCCC
ATTGGAATAAGATAACTGTGGAAACCCCTTTCAGATAAATACAAGCTAAGTAGCGAAGGTACCTTGGAAATATCT
AACATACAAATTGAAGACTCAGGAAGATACACATGTGTTGCCCAGAATGTCCAAGGGGCAGACACTCGGGTGGCA
ACAATTAAGGTTAACGGGACCCCTTCTGGATGGTACCCAGGTGCTAAAAATATACGTCAAGCAGACAGAATCCCAT
TCCATCTTAGTGTCTTGAAAGTTAATTCCAATGTCATGACGTCAAACCTTAAATGGTCTGTGCCACCATGAAG
ATTGATAACCCCTCACATAACATATACTGCCAGGGTCCCAGTCGATGTCCATGAATACAACCTAACGCATCTGCAG
CCTTCCACAGATTATGAAGTGTGTCTCACAGTGTCCAATATTCATCAGCAGACTCAAAGTCATGCGTAAATGTC
ACAACCAAAAATGCCGCCTTCGCAGTGGACATCTCTGATCAAGAAACCAGTACAGCCCTTGCTGCAGTAATGGGG
TCTATGTTTTGCCGTCAATTAGCCTTGCGTCCATTGCTGTGTACTTTGCCAAAAGATTTAAGAGAAAAAACTACCAC
CACTCATTA AAAAAGTATATGCAAAAACCTCTTCAATCCCACTAAATGAGCTGTACCCACCACTCATTAACCTC
TGGGAAGGTGACAGCGAGAAAGACAAAGATGGTTCTGCAGACACCAAGCCAACCCAGGTGACACATCCAGAAGC
TATTACATGTGGTAACTCAGAGGATATTTTGCTTCTGGTAGTAAGGAGCACAAAGACGTTTTTGTCTTTATTCTGC
AAAAGTGAACAAGTTGAAGACTTTTTGTATTTTTGACTTTGCTAGTTTGTGGCAGAGTGGAGAGGACGGGTGGATA
TTTCAAATTTTTTTAGTATAGCGTATCGCAAGGGTTTGACACGGCTGCCAGCGACTCTAGGCTTCCAGTCTGTGT
TTGGTTTTTTATTCTTATCATTATTATGATTGTTATTATATTATTTTATTTTAGTTGTTGTGCTAAACTCAAT
AATGCTGTTCTAACTACAGTGCTCAATAAAATGATTAATGACAGGAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
AAA

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FIGURE 512

MARMSFVIAACQLVLGLLMTSLTESSIONSECPQLCVCEIRPWFTPQSTYREATTVDCNDLRL
TRIPSNLSSDTQVLLLQSNNIAKTVDELQQLFNLTELDIFSQNNFTNIKEVGLANLTQLTTLHL
EENQITEMTDYCLQDLSNLQELYINHNQISTISAHAFAGLKNLLRLHLNSNKLKVIDSRWFDS
TPNLEILMIGENPVIGILDMNFKPLANLRSLVLAGMYLTDIPGNALVGGLDSLESLSFYDNKLV
KVPQLALQKVPNLKFLDLNKNPIHKIQEGDFKNMLRLKELGINNMGELVSVDYALDNLPELT
KLEATNNPKLSYIHRLAFRSVPALSLMLNNNALNAIYQKTVESLPNLREISIHNSNPLRCDV
IHWINSNKTNIIRFMEPLSMFCAMPPEYKQVKEVLIQDSSEQCLPMISHDSFPNRLNVDIGT
TVFLDCRAMAEPEPEIYWVTPIGNKITVETLSDKYKLSSEGTLEISNIQIEDSGRYTCVAQNV
QGADTRVATIKVNGTLLDGTQVLKIYVKQTESHSILVSWKVNSNVMTSNLKWSSATMKIDNPH
ITYTARVPVDVHEYNLTHLQPSTDYEVCLTVSNIHQQTQKSCVNVTTKNAFAVDISDQETST
ALAAVMGSMFAVISLASIAVYFAKRFRKKNYHHSLLKKYMQKTSSIPLNELYPPPLINLWEGDSE
KDKDGSADTKPTQVDTSRSYMW

Important features:**Signal peptide:**

Amino acids 1-25

Transmembrane domain:

Amino acids 508-530

N-glycosylation sites:Amino acids 69-73;96-100;106-110;117-121;385-389;517-521;
582-586;611-615**Tyrosine kinase phosphorylation site:**

Amino acids 573-582

N-myristoylation sites:

Amino acids 16-22;224-230;464-470;637-643;698-704

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FIGURE 513

GGGAGAGAGGATAAATAGCAGCGTGGCTTCCCTGGCTCCTCTCTGCATCCTTCCCGACCTTCC
CAGCAAT**ATG**CATCTTGACGTCTGGTCGGCTCCTGCTCCCTCCTTCTGCTACTGGGGGCCCT
GTCTGGATGGGCGGCCAGCGATGACCCCATTGAGAAGGTCATTGAAGGGATCAACCGAGGGCT
GAGCAATGCAGAGAGAGAGGTGGGCAAGGCCCTGGATGGCATCAACAGTGGAATCACGCATGC
CGGAAGGGAAGTGGAGAAGGTTTTCAACGGACTTAGCAACATGGGGAGCCACACCGGCAAGGA
GTTGGACAAAGGCGTCCAGGGGCTCAACCACGGCATGGACAAGGTTGCCCATGAGATCAACCA
TGGTATTGGACAAGCAGGAAAGGAAGCAGAGAAGCTTGGCCATGGGGTCAACAACGCTGCTGG
ACAGGCCGGGAAGGAAGCAGACAAAGCGGTCCAAGGGTTCCACACTGGGGTCCACCAGGCTGG
GAAGGAAGCAGAGAACTTGGCCAAGGGGTCAACCATGCTGCTGACCAGGCTGGAAAGGAAGT
GGAGAAGCTTGGCCAAGGTGCCCACCATGCTGCTGGCCAGGCCGGGAAGGAGCTGCAGAATGC
TCATAATGGGGTCAACCAAGCCAGCAAGGAGGCCAACCAGCTGCTGAATGGCAACCATCAAAG
CGGATCTTCCAGCCATCAAGGAGGGGGCCACAACCACGCCGTTAGCCTCTGGGGCCTCAGTCAA
CACGCCTTTCATCAACCTTCCCGCCCTGTGGAGGAGCGTCGCCAACATCATGCCCT**TAA**ACTGG
CATCCGGCCTTGCTGGGAGAATAATGTCGCCGTTGTCACATCAGCTGACATGACCTGGAGGGG
TTGGGGGTGGGGGACAGGTTTCTGAAATCCCTGAAGGGGGTGTACTGGGATTTGTGAATAAA
CTTGATACACCA

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FIGURE 514

MHLARLVGSCSLLLLLGALSGWAASDDPIEKVIEGINRGLSNAEREVVGKALDGINSGITHAGR
EVEKVFNGLSNMGSHTGKELDKGVQGLNHGMDKVAHEINHGIGQAGKEAEKLGHGVNNAAGQA
GKEADKAVQGFHTGVHQAGKEAEKLGQGVNHAADQAGKEVEKLGQGAHHAAGQAGKELQNAHN
GVNQASKEANQLLNGNHQSGSSSHQGGATTTPLASGASVNTPFINLPALWRSVANIMP

Important features:**Signal peptide:**

amino acids 1-25

Homologous region to circumsporozoite (CS) repeats:

amino acids 35-225

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FIGURE 515

CCCACGCGTCCGCCCACGCGTCCGGGTGCCACTCGCGCGCCGGCCGCGCTCCGGGCTTCTCTT
TTCCCTCCGACGCGCCACGGCTGCCCAGACATTCGGGTGCCGGGTCTGGAGAGCTCCCCGAA
CCCCTCCGCGGAGAGGAGCGAGGCGGCGCCAGGGTGGCCCCCGGGGCGCGCTTGGTCTCGGAG
AAGCGGGGACGAGGCCGAGGATGAGCGACTGAGGGCGACGCGGGCACTGACGCGAGTTGGGG
CCGCGACTACCGGCAGCTGACAGCGCGATGAGCGACTCCCCAGAGACGCCCTAGCCCCGGTGTG
CGCGCCAGGCGGAGCGCGCAGGTGGGGCTGGGCTGTTAGTGGTCCGCCCCACGCGGGTTCGCCG
GCCGGCCCAGGATGGGCGCTGGCAACCCGGGCCCCGCGCCCGCCGCTGCTACCCCTGCGCCCCG
TGCGAGCCCCGGCGTCCGGCCCCGCGCCCTGCGCTCATGGACGGCGGGTCCCGGTGGCGGGCGG
CGCCCCCGGGCTGTGAATGCGACTCGCCCCCTCGGCCGCGCTCCCCGCCCCGCCGCCGCCG
GACGTGGTAGGGGATGCCCAGCTCCACTGCGATGGCAGTTGGCGCGCTCTCCAGTTCCCTCCT
GGTCACCTGCTGCCTGATGGTGGCTCTGTGCAGTCCGAGCATCCCGCTGGAGAAGCTGGCCCA
GGCACCAGAGCAGCCGGGCCAGGAGAAGCGTGAGCACGCCACTCGGGACGGCCCCGGGGCGGGT
GAACGAGCTCGGGCGCCCCGGCGAGGGACGAGGGCGGCAGCGGCCGGGACTGGAAGAGCAAGAG
CGGCCGTGGGCTCGCCGGCCGTGAGCCGTGGAGCAAGCTGAAGCAGGCCTGGGTCTCCCAGGG
CGGGGGCGCCAAGGCCGGGGATCTGCAGGTCCGGCCCCGCGGGGACACCCCGCAGGCGGAAGC
CCTGGCCGCAGCCGCCAGGACGCGATTGGCCCGGAACTCGCGCCACGCCCGAGCCACCCGA
GGAGTACGTGTACCCGGACTACCGTGGCAAGGGCTGCGTGGACGAGAGCGGCTTCGTGTACGC
GATCGGGGAGAAGTTCGCGCCGGGCCCCCTCGGCCTGCCCGTGCTGTGCACCGAGGAGGGGCC
GCTGTGCGCGCAGCCCCAGTGCCCCAGGCTGCACCCGCGCTGCATCCACGTCGACACGAGCCA
GTGCTGCCCCGAGTGCAAGGAGAGGAAGAACTACTGCGAGTTCCGGGGCAAGACCTATCAGAC
TTTGGAGGAGTTCGTGGTGTCTCCATGCGAGAGGTGTGCTGTGAAGCCAACGGTGAGGTGCT
ATGCACAGTGTGAGCGTGTCCCCAGACGGAGTGTGTGGACCCTGTGTACGAGCCTGATCAGTG
CTGTCCCATCTGCAAAAATGGTCCAACTGCTTTGCAGAAACCGCGGTGATCCCTGCTGGCAG
AGAAGTGAAGACTGACGAGTGCACCATATGCCACTGTACTTATGAGGAAGGCACATGGAGAAT
CGAGCGGCAGGCCATGTGCACGAGACATGAATGCAGGCAAATGTAGACGCTTCCCAGAACACA
AACTCTGACTTTTTTCTAGAACATTTTACTGATGTGAACATTCTAGATGACTCTGGGAACATC
AGTCAAAGAAGACTTTTGATGAGGAATAATGGAAAATTGTTGGTACTTTTCCTTTTCTTGATA
ACAGTTACTACAACAGAAGGAAATGGATATATTTCAAACATCAACAAGAACTTTGGGCATAA
AATCCTTCTCTAAATAAATGTGCTATTTTCACAGTAAGTACACAAAAGTACACTATTATATAT
CAAATGTATTTCTATAATCCCTCCATTAGAGAGCTTATATAAGTGTTTTCTATAGATGCAGAT
TAAAAATGCTGTGTTGTCAACCGTCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

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FIGURE 516

MPSSTAMAVGALSSSLLVTCCLMVALCSPSIPLEKLAQAPEQPGQEKEHATRDGPGRVNELG
RPARDEGGSGRDWKS KSGRGLAGREPWSKLKQAWVSQGGGAKAGDLQVRPRGDT PQAEALAAA
AQDAIGPELAPTPEPPEEYVYPDYRGKGCVDSESGFVYAIGKEKFAPGPSACPCLCTEEGPLCAQ
PECPR LHPRCIHVDT SQCCPQCKERNYCEFRGKTYQTLEEFVVSPCERCRC EANGEVLCTVS
ACPQTECVDPVYEPDQCCPICKNGPNCFAETA V I PAGREVKTDECTICHCTYE EGTWRIERQA
MCTRHECRQM

Important features:**Signal peptide:**

amino acids 1-27

Transmembrane domain:

amino acids 11-30

Glycosaminoglycan attachment site.

amino acids 80-83

N-myristoylation sites.

amino acids 10-15, 102-107, 103-108

Cell attachment sequence.

amino acids 114-117

EGF-like domain cysteine pattern signature.

amino acids 176-187

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FIGURE 517

GGACAACCGTTGCTGGGTGTCCCAGGGCCTGAGGCAGGACGGTACTCCGCTGACACCTTCCCT
TTCGGCCTTGAGGTTCCCAGCCTGGTGGCCCCAGGACGTTCCGGTCGCATGGCAGAGTGCTAC
GGACGACGCCTATGAAAGCCCTTAGTCCTTCTAGTTGCGCTTTTGCTATGGCCTTCGTCTGTGC
CGGCTTATCCGAGCATAACTGTGACACCTGATGAAGAGCAAACTTGAATCATTATATACAAG
TTTTAGAGAACCTAGTACGAAGTGTTCCCTCTGGGGAGCCAGGTCGTGAGAAAAATCTAACT
CTCCAAACATGTTTATTCTATAGCATCAAAGGGATCAAAATTTAAGGAGCTAGTTACACATG
GAGACGCTTCAACTGAGAATGATGTTTTAACCAATCCTATCAGTGAAGAACTACAACCTTCC
CTACAGGAGGCTTCACACCGGAAATAGGAAAGAAAAACACACGGAAAGTACCCCATTTCTGGT
CGATCAAACCAAACAATGTTTCCATTGTTTTGCATGCAGAGGAACCTTATATTGAAAATGAAG
AGCCAGAGCCAGAGCCGGAGCCAGCTGCAAAACAACTGAGGCACCAAGAATGTTGCCAGTTG
TACTGAATCATCTACAAGTCCATATGTTACCTCATACAAGTCACCTGTCACCACTTTAGATA
AGAGCACTGGCATTGAGATCTCTACAGAATCAGAAGATGTTTCCTCAGCTCTCAGGTGAACTG
CGATAGAAAAACCCGAAGAGTTTGGAAGCACCCAGAGAGTTGGAATAATGATGACATTTTGA
AAAAATTTTAGATATTAATTCACAAGTGCAACAGGCACTTCTTAGTGACACCAGCAACCCAG
CATATAGAGAAGATATTGAAGCCTCTAAAGATCACCTAAAACGAAGCCTTGCTCTAGCAGCAG
CAGCAGAACATAAATTAAAAACAATGTATAAGTCCCAGTTATTGCCAGTAGGACGAACAAGTA
ATAAAATTGATGACATCGAACTGTTATTAACATGCTGTGTAATTCTAGATCTAACTCTATG
AATATTTAGATATTAAATGTGTTCCACCAGAGATGAGAGAAAAAGCTGCTACAGTATTCAATA
CATTAaaaaatATGTGTAGATCAAGGAGAGTCACAGCCTTATTAAAAGTTTATTAAACAATAA
TATAAAATTTTAAACCTACTTGATATTCCATAACAAAGCTGATTTAAGCAAACCTGCATTTTT
TCACAGGAGAAATAATCATATTCGTAATTTCAAAGTTGTATAAAATATTTTCTATTGTAGT
TCAAATGTGCCAACATCTTTATGTGTGTCATGTGTTATGAACAATTTTCATATGCACTAAAAACC
TAATTTAAATAAAATTTTGGTTCAGGAAAAA

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FIGURE 518

MKPLVLLVALLLWPSSVPAYPSITVTPDEEQNLNHYIQVLENLVRSVPSGEPGREKKSNSPKH
VYSIASKGSKFKELVTHGDASTENDVLNPISEETTTFTPTGGFTPEIGKKKHTESTPFWSIKP
NNVSIVLHAEOPYIENEEPEPEPEPAAKQTEAPRMLPVVTESSSTSPYVTSYKSPVTTLDKSTG
IEISTESEDVPQLSGETAIEKPEEFGKHPESWNDDILKKILDINSQVQQALLSDTSNPAYRE
DIEASKDHLKRSLALAAAAEHKLKTMYSQLLPVGRTSNKIDDIETVINMLCNSRSKLYEYLD
IKCVPPEMREKAATVFNTLKNMCRSRRVTALLKVY

Important features:**Signal peptide:**

amino acids 1-19

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FIGURE 519

CGGCTCGAGTGCAGCTGTGGGGAGATTTTCAGTGCATTGCCTCCCCTGGGTGCTCTTCATCTTG
GATTTGAAAGTTGAGAGCAGC**ATG**TTTTTGCCCACTGAAACTCATCCTGCTGCCAGTGTTACTG
GATTATTCCTTGGGCCTGAATGACTTGAATGTTTCCCCGCCTGAGCTAACAGTCCATGTGGGT
GATTCAGCTCTGATGGGATGTGTTTTCCAGAGCACAGAAGACAAATGTATATTCAAGATAGAC
TGGACTCTGTCACCAGGAGAGCACGCCAAGGACGAATATGTGCTATACTATTACTCCAATCTC
AGTGTGCCTATTGGGCGCTTCCAGAACCGCGTACACTTGATGGGGGACATCTTATGCAATGAT
GGCTCTCTCCTGCTCCAAGATGTGCAAGAGGCTGACCAGGGAACCTATATCTGTGAAATCCGC
CTCAAAGGGGAGAGCCAGGTGTTCAAGAAGGCGGTGGTACTGCATGTGCTTCCAGAGGAGCCC
AAAGAGCTCATGGTCCATGTGGGTGGATTGATTCAGATGGGATGTGTTTTCCAGAGCACAGAA
GTGAAACACGTGACCAAGGTAGAATGGATATTTTCAGGACGGCGCGCAAAGGAGGAGATTGTA
TTTCGTTACTACCACAACTCAGGATGTCTGTGGAGTACTCCCAGAGCTGGGGCCACTTCCAG
AATCGTGTGAACCTGGTGGGGGACATTTTCCGCAATGACGGTTCCATCATGCTTCAAGGAGTG
AGGGAGTCAGATGGAGGAACTACACCTGCAGTATCCACCTAGGGAACCTGGTGTTCAGAAA
ACCATTGTGCTGCATGTCAGCCCGGAAGAGCCTCGAACACTGGTGACCCCGGCAGCCCTGAGG
CCTCTGGTCTTGGGTGGTAATCAGTTGGTGATCATTGTGGGAATTGTCTGTGCCACAATCCTG
CTGCTCCCTGTTCTGATATTGATCGTGAAGAAGACCTGTGGAATAAGAGTTCAGTGAATTCT
ACAGTCTTGGTGAAGAACACGAAGAAGACTAATCCAGAGATAAAAGAAAAACCCTGCCATTTT
GAAAGATGTGAAGGGGAGAAACACATTTACTCCCCAATAATTGTACGGGAGGTGATCGAGGAA
GAAGAACCAAGTGAAAAATCAGAGGCCACCTACATGACCATGCACCCAGTTTGGCCTTCTCTG
AGGTCAGATCGGAACAACCTCACTTGAAAAAAGTCAGGTGGGGGAATGCCAAAAACACAGCAA
GCCTTT**TGA**GAGAAGATGGAGAGTCCCTTCATCTCAGCAGCGGTGGAGACTCTCTCCTGTGTGT
GTCCTGGGCCACTCTACCAGTGATTTCAGACTCCCGCTCTCCAGCTGTCCTCCTGTCTCATT
GTTTGGTCAATACACTGAAGATGGAGAATTTGGAGCCTGGCAGAGAGACTGGACAGCTCTGGA
GGAACAGGCCTGCTGAGGGGAGGGGAGCATGGACTTGGCCTCTGGAGTGGGACACTGGCCCTG
GGAACCAGGCTGAGCTGAGTGGCCTCAAACCCCCCGTTGGATCAGACCCTCCTGTGGGCAGGG
TTCTTAGTGGATGAGTTACTGGGAAGAATCAGAGATAAAACCAACCCAAATCAA

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FIGURE 520

MFCPLKLILLPVLLDYSLGLNDLNVSPPELTVHVGDSALMGCVFQSTEDKCI FKIDWTLS PGE
HAKDEYVLYYYSNLSVPIGRFQNRVHLMGDILCNDGSLLLQDVQEADQGT YICEIRLKGESQV
FKKAVVLHVLPEEPKELMVHVGGLIQMGCVFQSTEVKHVTKVEWIFSGRRAKEEIVFRYYHKL
RMSVEYSQSWG HFQNRVNLVGDIFRNDGSIMLQGVRES DGGNYTCS IHLGNLVFKKTIVLHVS
PEEPRTLVT PAALRPLVLGGNQLVIIVGIVCATILLLPVLILIVKKT CGNKSSVNSTVLVKNT
KKTNP EIKEKPC HFERCEGEKHIYSPIIVREVIEEEEPSEKSEATYMTMHPVWPSLRSDRNNS
LEKKSGGGMPKTQQAF

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FIGURE 521

CTATGAAGAAGCTTCCTGGAAAACAATAAGCAAAGGAAAACAAATGTGTCCCATCTCACATGG
TTCTACCCTACTAAAGACAGGAAGATCATAAACTGACAGATACTGAAATTGTAAGAGTTGGAA
ACTACATTTTGCAAAGTCATTGAACTCTGAGCTCAGTTGCAGTACTCGGGAAGCC**ATG**CAGGA
TGAAGATGGATACATCACCTTAAATATTAAAACTCGGAAACCAGCTCTCGTCTCCGTTGGCCC
TGCATCCTCCTCCTGGTGGCGTGTGATGGCTTTGATTCTGCTGATCCTGTGCGTGGGGATGGT
TGTCGGGCTGGTGGCTCTGGGGATTTGGTCTGTTCATGCAGCGCAATTACCTACAAGATGAGAA
TGAAAATCGCACAGGAACCTCTGCAACAATTAGCAAAGCGCTTCTGTCAATATGTGGTAAAACA
ATCAGAACTAAAGGGCACTTTCAAAGGTCATAAATGCAGCCCCTGTGACACAACTGGAGATA
TTATGGAGATAGCTGCTATGGGTTCTTCAGGCACAACTTAACATGGGAAGAGAGTAAGCAGTA
CTGCACTGACATGAATGCTACTCTCCTGAAGATTGACAACCGGAACATTGTGGAGTACATCAA
AGCCAGGACTCATTTAATTCGTTGGGTCGGATTATCTCGCCAGAAGTCGAATGAGGTCTGGAA
GTGGGAGGATGGCTCGGTTATCTCAGAAAATATGTTTGAGTTTTTGGGAAGATGGAAAAGGAAA
TATGAATTGTGCTTATTTTCATAATGGGAAAATGCACCCTACCTTCTGTGAGAACAAACATTA
TTTAATGTGTGAGAGGAAGGCTGGCATGACCAAGGTGGACCAACTACCT**TAA**TGCAAAGAGGT
GGACAGGATAACACAGATAAGGGCTTTATTGTACAATAAAAGATATGTATGAATGCATCAGTA
GCTGAAAAAAAAAAAAA

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FIGURE 522

MQDEMGYITLNIKTRKPALVSVGPASSSWWRVMALILLILCVGMVVGLVALGIWSVMQRNYLQ
DENENRTGTLQQLAKRFCQYVVKQSELKGTFKGHKCSPCDTNWRYYGDSYGFRRHNLWEES
KQYCTDMNATLLKIDNRNIVEYIKARTHLIRWVGLSRQKSNEVKKWEDGSVISENMFEFLEDG
KGNMNCAYFHNGKMHPTFCENKHYLMCERKAGMTKVDQLP

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FIGURE 523

CAGCAGTGGTCTCTCAGTCCTCTCAAAGCAAGGAAAGAGTACTGTGTGCTGAGAGACC**ATG**GC
AAAGAATCCTCCAGAGAATTGTGAAGACTGTCACATTCTAAATGCAGAAGCTTTTAAATCCAA
GAAAATATGTAAATCACTTAAGATTTGTGGACTGGTGTTTGGTATCCTGGCCCTAACTCTAAT
TGTCCTGTTTTGGGGGAGCAAGCACTTCTGGCCGGAGGTACCCAAAAAGCCTATGACATGGA
GCACACTTTCTACAGCAATGGAGAGAAGAAGAAGATTTACATGGAAATTGATCCTGTGACCAG
AACTGAAATATTCAGAAGCGGAAATGGCACTGATGAAACATTGGAAGTGCACGACTTTAAAAA
CGGATACACTGGCATCTACTTCGTGGGTCTTCAAAAATGTTTTATCAAACTCAGATTAAAGT
GATTCCTGAATTTTCTGAACCAGAAGAGGAAATAGATGAGAATGAAGAAATTACCACAACCTTT
CTTTGAACAGTCAGTGATTTGGGTCCCAGCAGAAAAGCCTATTGAAAACCGAGATTTTCTTAA
AAATTCCAAAATTCTGGAGATTTGTGATAACGTGACCATGTATTGGATCAATCCCACTCTAAT
ATCAGTTTCTGAGTTACAAGACTTTGAGGAGGAGGGAGAAGATCTTCACTTTCCTGCCAACGA
AAAAAAGGGATTGAACAAAATGAACAGTGGGTGGTCCCTCAAGTGAAAGTAGAGAAGACCCG
TCACGCCAGACAAGCAAGTGAGGAAGAACTTCCAATAAATGACTATACTGAAAATGGAATAGA
ATTTGATCCCATGCTGGATGAGAGAGGTTATTGTTGTATTTACTGCCGTCGAGGCAACCGCTA
TTGCCGCCGCGTCTGTGAACCTTTACTAGGCTACTACCCATATCCATACTGCTACCAAGGAGG
ACGAGTCATCTGTCTGTCATCATGCCTTGTAAGTGGTGGGTGGCCCGCATGCTGGGGAGGGT
CTAATAGGAGGTTTGAGCTCAAATGCTTAACTGCTGGCAACATATAATAAATGCATGCTATT
CAATGAATTTCTGCCTATGAGGCATCTGGCCCCTGGTAGCCAGCTCTCCAGAATTACTTGTAG
GTAATTCCTCTCTTCATGTTCTAATAAACTTCTACATTATCACCAAAAAAAAAAAAAAAAAA

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FIGURE 524

MAKNPPENCEDCHILNAEAFKSKKICKSLKICGLVFGILALTLLIVLFWGSKHFWPEVPPKKAYD
MEHTFYSNGEKKKIYMEIDPVTRTEIFRSGNGTDETLEVHDFKNGYTGIYFVGLQKCFIKTQI
KVIPEFSEPEEEIDENEEITTTFFEQSVIWVPAEKPIENRDFLKNSKILEICDNVTMYWINPT
LISVSELQDFEEEGEDLHFPA NEKKGIEQNEQWVVPQVKVEKTRHARQASEEELPINDYTENG
IEFDPMLDERGYCCIIYCRGNRYCRRVCEPLLGYYPYPYCYQGGRVICRVIMPCNWWVARMLGRV

Important features:**Signal peptide:**

amino acids 1-40

Transmembrane domain:

amino acids 25-47 (type II)

N-glycosylation sites.

amino acids 94-97, 180-183

Glycosaminoglycan attachment sites.

amino acids 92-95, 70-73, 85-88, 133-136, 148-151, 192-195, 239-242

N-myristoylation sites.

amino acids 33-38, 95-100, 116-121, 215-220, 272-277

Microbodies C-terminal targeting signal.

amino acids 315-317

Cytochrome c family heme-binding site signature.

amino acids 9-14

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FIGURE 525

AGTGACAATCTCAGAGCAGCTTCTACACCACAGCCATTTCCAGCATGAAAGATCACTGGGGGTC
TCCTTCTGCTCTGTACAGTGGTCTATTTCTGTAGCAGCTCAGAAGCTGCTAGTCTGTCTCCAA
AAAAAGTGGACTGCAGCATTTACAAGAAGTATCCAGTGGTGGCCATCCCCTGCCCCATCACAT
ACCTACCAGTTTGTGGTTCTGACTACATCACCTATGGGAATGAATGTCACCTGTGTACCGAGA
GCTTGAAAAGTAATGGAAGAGTTCAGTTTCTTCACGATGGAAGTTGCTAAATTCTCCATGGAC
ATAGAGAGAAAGGAATGATATTCTCATCATCATCTTCATCATCCCAGGCTCTGACTGAGTTTC
TTTCAGTTTTTACTGATGTTCTGGGTGGGGGACAGAGCCAGATTCAGAGTAATCTTGACTGAAT
GGAGAAAGTTTCTGTGCTACCCCTACAAACCCATGCCTCACTGACAGACCAGCATTTTTTTTTT
TAACACGTCAATAAAAAAATAATCTCCCAGA

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FIGURE 526

MKITGGLLLLCTVVYFCSSSEAASLSPKKVDCSIYKKYPVVAIPCPITYLPVCGSDYITYGNE
CHLCTESLKSNGRVQFLHDGSC

Important features:

Signal peptide:

amino acids 1-19

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FIGURE 527

CGACG**ATG**CTACGCGCGCCCGGCTGCCTCCTCCGGACCTCCGTAGCGCCTGCCGCGGCCCTGG
CTGCGGCGCTGCTCTCGTCGCTTGCGCGCTGCTCTCTTCTAGAGCCGAGGGACCCGGTGGCCT
CGTCGCTCAGCCCCCTATTTTCGGCACCAAGACTCGCTACGAGGATGTCAACCCCGTGCTATTGT
CGGGCCCCGAGGCTCCGTGGCGGGACCCCTGAGCTGCTGGAGGGGACCTGCACCCCGGTGCAGC
TGGTCGCCCCTCATTCGCCACGGCACCCCGCTACCCACGGTCAAACAGATCCGCAAGCTGAGGC
AGCTGCACGGGTGCTGCAGGCCCGCGGGTCCAGGGATGGCGGGGCTAGTAGTACCGGCAGCC
GCGACCTGGGTGCAGCGCTGGCCGACTGGCCTTTGTGGTACGCGGACTGGATGGACGGGCAGC
TAGTAGAGAAGGGACGGCAGGATATGCGACAGCTGGCGCTGCGTCTGGCCTCGCTCTTCCCGG
CCCTTTTTCAGCCGTGAGAACTACGGCCGCTGCGGCTCATCACCAGTTCCAAGCACCGCTGCA
TGGATAGCAGCGCCGCTTCTGTCAGGGGCTGTGGCAGCACTACCACCCTGGCTTGCCGCCGC
CGGACGTCGAGATATGGAGTTTGGACCTCCAACAGTTAATGATAAACTAATGAGATTTTTTG
ATCACTGTGAGAAGTTTTTAAGTAGAAAAAATGCTACAGCTCTTTATCACGTGGAAG
CCTTCAAACTGGACCAGAAATGCAGAACATTTTAAAAAAGTTGCAGCTACTTTGCAAGTGC
CAGTAAATGATTTAAATGCAGATTTAATTCAAGTAGCCTTTTTACCTGTTTCAATTTGACCTGG
CAATTAAAGGTGTTAAATCTCCTTGGTGTGATGTTTTTGACATAGATGATGCAAAGGTATTAG
AATATTTAAATGATCTGAAACAATATTGGAAAAGAGGATATGGGTATACTATTAACAGTCGAT
CCAGCTGCACCTTGTTTCAGGATATCTTTCAGCACTTGGACAAAGCAGTTGAACAGAAACAAA
GGTCTCAGCCAATTTCTTCTCCAGTCATCCTCCAGTTTGGTCATGCAGAGACTCTTCTTCCAC
TGCTTTTCTCTCATGGGCTACTTCAAAGACAAGGAACCCCTAACAGCGTACAATTACAAAAAAC
AAATGCATCGGAAGTTCCGAAGTGGTCTCATTGTACCTTATGCCTCGAACCTGATATTTGTGC
TTTACCACTGTGAAAATGCTAAGACTCCTAAAGAACAATTCCGAGTGCAGATGTTATTAAATG
AAAAGGTGTTACCTTTGGCTTACTCACAAGAACTGTTTCATTTTATGAAGATCTGAAGAACC
ACTACAAGGACATCCTTCAGAGTTGTCAAACCAGTGAAGAAATGTGAATTAGCAAGGGCTAACA
GTACATCTGATGAACTA**TGA**GTAAGTGAAGAACATTTTTTAATTCTTTAGGAATCTGCAATGAG
TGATTACATGCTTGTAATAGGTAGGCAATTCCTTGATTACAGGAAGCTTTTATATTACTTGAG
TATTTCTGTCTTTTCACAGAAAAACATTGGGTTTCTCTCTGGGTTTGGACATGAAATGTAAGA
AAAGATTTTTCACTGGAGCAGCTCTCTTAAGGAGAAACAAATCTATTTAGAGAAACAGCTGGC
CCTGCAAAATGTTTACAGAAATGAAATTCCTTCTACTTATATAAGAAATCTCACACTGAGATAG
AATTGTGATTTTATAATAACACTTGAAAAGTGCTGGAGTAACAAAATATCTCAGTTGGACCAT
CCTTAACCTTGATTGAACTGTCTAGGAACCTTTACAGATTGTTCTGCAGTTCTCTCTTCTTTCC
TCAGGTAGGACAGCTCTAGCATTTTCTTAATCAGGAATATTGTGGTAAGCTGGGAGTATCACT
CTGGAAGAAAGTAACATCTCCAGATGAGAATTTGAAACAAGAAACAGAGTGTTGTAAAAGGAC
ACCTTCACTGAAGCAAGTCGGAAAGTACAATGAAAATAAATATTTTTGGTATTTATTTATGAA
ATATTTGAACATTTTTTCAATAATTCCTTTTTTACTTCTAGGAAGTCTCAAAAGACCATCTTAA
ATTATTATATGTTTGGACAATTAGCAACAAGTCAGATAGTTAGAATCGAAGTTTTTCAAATCC
ATTGCTTAGCTAACTTTTTTCATTCTGTCACTTGGCTTCGATTTTTTATATTTTCTATTATATG
AAATGTATCTTTTGGTTGTTTGATTTTTCTTTCTTTCTTTGTAAATAGTTCTGAGTTCTGTCA
AATGCCGTGAAAGTATTTGCTATAATAAGAAAATTCTTGTGACTTTAAAAA

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FIGURE 528

MLRAPGCLLRTSVAPAAALAAALLSSLARCSLLEPRDPVASSLSFYFGTKTRYEDVNPVLLSG
PEAPWRDPELLEGTCTPVQLVALIRHGTRYPTVKQIRKLRQLHGLLQARGSRDGGASSTGSRD
LGAALADWPLWYADWMDGQLVEKGRQDMRQLALRLASLFPALFSRENYGRLRLITSSKHRCMD
SSAAFLQGLWQHYHPGLPPPDVADMEFGPPTVNDKLMRFFDHCEKFLTEVEKNATALYHVEAF
KTGPEMQNILKKVAATLQVPVNDLNADLIQVAFFTCSEDLAIKGVKSPWCDVFDIDDAKVLEY
LNDLKQYWKRQGYGYTINSRSSCTLFQDIFQHLDKAVEQKQRSQPISSPVILQFGHAETLLPLL
SLMGYFKDKEPLTAYNYKKQMRKFRSGLIVPYASNLI FVLYHCENAKTPKEQFRVQMLLNEK
VLPLAYSQETVSFYEDLKNHYKDILQSCQTSEECELARANSTSDDEL

Important features:**Signal sequence**

amino acids 1-30

N-glycosylation sites.

amino acids 242-246, 481-485

N-myristoylation sites.

amino acids 107-113, 113-119, 117-123, 118-124, 128-134

Endoplasmic reticulum targeting sequence.

amino acids 484-489

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FIGURE 529

GGAGAGCCGCGGCTGGGACCGGAGTGGGGAGCGCGGCGTGGAGGTGCCACCCGGCGCGGGTGG
CGGAGAGATCAGAAAGCCTCTTCCCCAAGCCGAGCCAACCTCAGCGGGGACCCGGGCTCAGGGA
CGCGGCGGCGGCGGCGGCGGCGACTGCAGTGGCTGGACGATGGCAGCGTCCGCCGGAGCCGGGGCG
GTGATTGCAGCCCCAGACAGCCGGCGCTGGCTGTGGTTCGGTGCTGGCGGCGGCGCTTGGGCTC
TTGACAGCTGGAGTATCAGCCTTGGAAGTATATACGCCAAAAGAAATCTTTCGTGGCAAATGGT
ACACAAGGGAAGCTGACCTGCAAGTTCAAGTCTACTAGTACGACTGGCGGGTTGACCTCAGTC
TCCTGGAGCTTCCAGCCAGAGGGGGCCGACACTACTGTGTCTGTTTTTCCACTACTCCCAAGGG
CAAGTGTACCTTGGGAATTATCCACCATTATAAGACAGAATCAGCTGGGCTGGAGACCTTGAC
AAGAAAGATGCATCAATCAACATAGAAAATATGCAGTTTATACACAATGGCACCTATATCTGT
GATGTCAAAAACCTCCTGACATCGTTGTCCAGCCTGGACACATTAGGCTCTATGTCTGTAGAA
AAAGAGAATTTGCCTGTGTTTCCAGTTTGGGTAGTGGTGGGCATAGTTACTGCTGTGGTCTTA
GGTCTCACTCTGCTCATCAGCATGATTCTGGCTGTCCTCTATAGAAGGAAAACTCTAAACGG
GATTACACTGGCTGCAGTACATCAGAGAGTTTGTCCAGGTTAAGCAGGCTCCTCGGAAGTCC
CCCTCCGACACTGAGGGTCTTGTAAGAGTCTGCCTTCTGGATCTCACCAGGGCCCAGTCATA
TATGCACAGTTAGACCACTCCGGCGGACATCACAGTGACAAGATTAACAAGTCAGAGTCTGTG
GTGTATGCGGATATCCGAAAGAATTAAAGAGAATACCTAGAACATATCCTCAGCAAGAAACAAA
ACCAAATGGACTCTCGTGCAGAAAATGTAGCCCATTAACCATGTAGCCTTGGAGACCCAGG
CAAGGACAAGTACACGTGTACTCACAGAGGGAGAGAAAGATGTGTACAAAGGATATGTATAAA
TATTCTATTTAGTCATCCTGATATGAGGAGCCAGTGTTCATGATGAAAAGATGGTATGATTC
TACATATGTACCCATTGTCTTGCTGTTTTTGTACTTTCTTTTCAGGTCATTTACAATTGGGAG
ATTTCAGAAACATTCCTTTACCATCATTTAGAAATGGTTTGCCTTAATGGAGACAATAGCAG
ATCCTGTAGTATTTCCAGTAGACATGGCCTTTTAATCTAAGGGCTTAAGACTGATTAGTCTTA
GCATTTACTGTAGTTGGAGGATGGAGATGCTATGATGGAAGCATACCCAGGGTGGCCTTTAGC
ACAGTATCAGTACCATTTATTTGTCTGCCGCTTTTAAAAAATACCCATTGGCTATGCCACTTG
AAAACAATTTGAGAAGTTTTTTTTGAAGTTTTTCTCACTAAAATATGGGGCAATTGTTAGCCTT
ACATGTTGTGTAGACTTACTTTAAGTTTGCACCCTTGAAATGTGTATATCAATTTCTGGATT
CATAATAGCAAGATTAGCAAAGGATAAATGCCGAAGGTCACCTCATTCTGGACACAGTTGGAT
CAATACTGATTAAGTAGAAAATCCAAGCTTTGCTTGAGAACTTTTGTAACTGGAGAGTAAAA
AGTATCGGTTTTTA

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FIGURE 530

MAASAGAGAVIAAPDSRRWLWSVLAAALGLLTAGVSALEVYTPKEIFVANGTQGKLTCKFKST
STTGGLTSVSWSFQPEGADTTVSFFHYSQGQVYLGNYPPFKDRISWAGDLDDKSDASINIENMQ
FIHNGTYICDVKNPPDIVVQPGHIRLYVVEKENLPVFPVWVVVGIVTAVVLGLTLLISMILAV
LYRRKNSKRDTGCGSTSESLSPVKQAPRKSPSDTEGLVKSLPSGSHQGPVIYAQLDHSGGHHS
DKINKSESVVYADIRKN

Important features:**Signal peptide:**

amino acids 1-37

Transmembrane domain:

amino acids 161-183

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FIGURE 531

GTGACACTATAGAAGAGCTATGACGTCGCATGCACGCGTACGTAAGCTCGGAATTCGGCTCGA
GGCTGGTGGGAAGAAGCCGAG**ATG**GCGGCAGCCAGCGCTGGGGCAACCCGGCTGCTCCTGCTC
TTGCTGATGGCGGTAGCAGCGCCCAGTCGAGCCCGGGGCAGCGGCTGCCGGGCCGGGACTGGT
GCGCGAGGGGCTGGGGCGGAAGGTCGAGAGGGCGAGGCCTGTGGCACGGTGGGGCTGCTGCTG
GAGCACTCATTTGAGATCGATGACAGTGCCAACTTCCGGAAGCGGGGCTCACTGCTCTGGAAC
CAGCAGGATGGTACCTTGTCCTGTACAGCGGCAGCTCAGCGAGGAGGAGCGGGGCCGACTC
CGGGATGTGGCAGCCCTGAATGGCCTGTACCGGGTCCGGATCCCAAGGCGACCCGGGGCCCTG
GATGGCCTGGAAGCTGGTGGCTATGTCTCCTCCTTTGTCCCTGCGTGCTCCCTGGTGGAGTCG
CACCTGTCGGACCAGCTGACCCTGCACGTGGATGTGGCCGGCAACGTGGTGGGCGTGTCGGTG
GTGACGCACCCCGGGGGCTGCCGGGGCCATGAGGTGGAGGACGTGGACCTGGAGCTGTTCAAC
ACCTCGGTGCAGCTGCAGCCGCCACCACAGCCCCAGGCCCTGAGACGGCGGCCTTCATTGAG
CGCCTGGAGATGGAACAGGCCCAGAAGGCCAAGAACCCCCAGGAGCAGAAGTCCTTCTTCGCC
AAATACTGGATGTACATCATTTCCCGTCGTCCTGTTCCCTCATGATGTCAGGAGCGCCAGACACC
GGGGGCCAGGGTGGGGGTGGGGGTGGGGGTGGTGGTGGGGGTAGTGGCCTTTGCTGTGTGCCA
CCCTCCCTG**TAA**GTCTATTTAAAAACATCGACGATACATTGAAATGTGTGAACGTTTTGAAAA
GCTACAGCTTCCAGCAGCCAAAAGCAACTGTTGTTTTGGCAAGACGGTCCTGATGTACAAGCT
TGATTGAAATTCCTGCTCACTTGATACGTTATTAGAAACCCAAGGAATGGCTGTCCCCATC
CTCATGTGGCTGTGTGGAGCTCAGCTGTGTTGTGTGGCAGTTTATTAAACTGTCCCCCAGATC
GACACGCAAAAAAAAAA

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FIGURE 532

MAAASAGATRLLLLLLMAVAAPSRARGSGCRAGTGARGAGAEGREGEACGTVGLLLEHSFEID
DSANFRKRGSLLWNQQDGTLSLSQRQLSEEERGRLRDVAALNGLYRVRI PRRPGALDGLEAGG
YVSSFVPACSLVESHLSDQLTLHVDVAGNVVGVSVVTHPGGCRGHEVEDVDLELFNTSVQLQP
PTTAPGPETA AFIERLEMEQAQKAKNPQEQKSFFAKYWYIIPVVLFLMMSGAPDTGGQGGGG
GGGGGGGSGLCCVPPSL

Important features:**Signal peptide:**

amino acids 1-24

Transmembrane domain:

amino acids 226-243

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FIGURE 534

MELALLCGLVVMAGVPIPIQGILNLNKMVKQVTGKMPILSYWPYGCHCGLGGRGQPKDATDWC
CQTHDCCYDHLKTQGCGIYKDNNKSSIHCMDSLQRYCLMAVFNVIIYLENEDSE

Important features:**Signal peptide:**

amino acids 1-17

Transmembrane domain:

amino acids 1-24

N-glycosylation site.

amino acids 86-89

N-myristoylation sites.

amino acids 20-25, 45-50

Phospholipase A2 histidine active site.

amino acids 63-70

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FIGURE 535

GCTGAGCGTGTGCGCGGTACGGGGCTCTCCTGCCTTCTGGGCTCCAACGCAGCTCTGTGGCTG
AACTGGGTGCTCATCACGGGAAGTGTGGGCTATGGAATACAGATGTGGCAGCTCAGGTAGCC
CCAAATTGCCTGGAAGAATACATCATGTTTTTCGATAAGAAGAAATTGTAGGATCCAGTTTTT
TTTTTAACCGCCCCCTCCCCACCCCCCAAAAAAAGTGTAAAGATGCAAAAACGTAATATCCAT
GAAGATCCTATTACCTAGGAAGATTTTGATGTTTTGCTGCGAATGCGGTGTTGGGATTTATTT
GTTCTTGGAGTGTTCTGCGTGGCTGGCAAAGAATAATGTTCCAAAATCGGTCCATCTCCCAAG
GGGTCCAATTTTTCTTCTGCGTGGTGTGAGCGAGCCCTGACTCACTACAGTGCAGCTGACAGGGG
CTGTCATGCAACTGGCCCCCTAAGCCAAAGCAAAAGACCTAAGGACGACCTTTGAACAATACAA
AGG**ATG**GGTTTCAATGTAATTAGGCTACTGAGCGGATCAGCTGTAGCACTGGTTATAGCCCCC
ACTGTCTTACTGACAATGCTTTCTTCTGCCGAACGAGGATGCCCTAAGGGCTGTAGGTGTGAA
GGCAAAATGGTATATTGTGAATCTCAGAAATTACAGGAGATACCCCTCAAGTATATCTGCTGGT
TGCTTAGGTTTGTCCCTTCGCTATAACAGCCTTCAAAAAGTAAAGTATAATCAATTTAAAGGG
CTCAACCAGCTCACCTGGCTATACCTTGACCATAACCATATCAGCAATATTGACGAAAATGCT
TTTAATGGAATACGCAGACTCAAAGAGCTGATTCTTAGTTCCAATAGAATCTCCTATTTTTCTT
AACAATACCTTCAGACCTGTGACAAATTTACGGAAGTGGATCTGTCCTATAATCAGCTGCAT
TCTCTGGGATCTGAACAGTTTCGGGGCTTGCGGAAGCTGCTGAGTTTACATTTACGGTCTAAC
TCCCTGAGAACCATCCCTGTGCGAATATTCCAAGACTGCCGCAACCTGGAAGTTTTGGACCTG
GGATATAACCGGATCCGAAGTTTAGCCAGGAATGTCTTTGCTGGCATGATCAGACTCAAAGAA
CTTCACCTGGAGCACAATCAATTTTCCAAGCTCAACCTGGCCCTTTTTTCCAAGGTTGGTCAGC
CTTCAGAACCTTTACTTGCAGTGGAATAAAATCAGTGTCATAGGACAGACCATGTCTGGACC
TGGAGCTCCTTACAAAGGCTTGATTTATCAGGCAATGAGATCGAAGCTTTCAGTGGACCCAGT
GTTTTCCAGTGTGTCCCGAATCTGCAGCGCCTCAACCTGGATTCCAACAAGCTCACATTTATT
GGTCAAGAGATTTTGGATTCTTGGATATCCCTCAATGACATCAGTCTTGCTGGGAATATATGG
GAATGCAGCAGAAATATTTGCTCCCTTGTAAGTGGCTGAAAAGTTTTAAAGGTCTAAGGGAG
AATACAATTATCTGTGCCAGTCCCCAAAGAGCTGCAAGGAGTAAATGTGATCGATGCAGTGAAG
AACTACAGCATCTGTGGCAAAAGTACTACAGAGAGGTTTGATCTGGCCAGGGCTCTCCCAAAG
CCGACGTTTAAGCCCAAGCTCCCCAGGCCGAAGCATGAGAGCAAACCCCTTTGCCCCCGACG
GTGGGAGCCACAGAGCCCCGGCCAGAGACCGATGCTGACGCCGAGCACATCTCTTTCCATAAA
ATCATCGCGGGCAGCGTGGCGCTTTTCCTGTCCGTGCTCGTCATCCTGCTGGTTATCTACGTG
TCATGGAAGCGGTACCCTGCGAGCATGAAGCAGCTGCAGCAGCGCTCCCTCATGCGAAGGCAC
AGGAAAAAGAAAAGACAGTCCCTAAAGCAAATGACTCCCAGCACCCAGGAATTTTATGTAGAT
TATAAACCCACCAACACGGAGACCAGCGAGATGCTGCTGAATGGGACGGGACCCCTGCACCTAT
AACAAATCGGGCTCCAGGGAGTGTGAGGTAT**TGA**ACCATTGTGATAAAAAGAGCTCTTAAAGC
TGGGAAATAAGTGGTGCTTTATTGAACTCTGGTGACTATCAAGGGAACGCGATGCCCCCCTC
CCCTTCCCTCTCCCTCTCACTTTGGTGGCAAGATCCTTCCTTGTCGTTTTAGTGCAATTCATA
ATACTGGTCATTTTCCCTCTCATACATAATCAACCCATTGAAATTTAAATACCACAATCAATGT
GAAGCTTGAAGTCCGGTTTAAATATAATACCTATTGTATAAGACCCCTTACTGATTCCATTAAT
GTCGCATTTGTTTTAAGATAAACTTCTTTCATAGGTAAAAA

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FIGURE 536

MGFNVIRLLSGSAVALVIAPTVLTLMLSSAERGCPKGCRCEGKMVYCESQKLQEIPSSISAGC
LGLSLRYNSLQKLKYNQFKGLNQLTWLYLDHNNHISNIDENAFNGIRRLKELILSSNRISYFLN
NTFRPVNTLRNLDLSYNQLHSLGSEQFRGLRKLLSLHLRSNSLRTPVRI FQDCRNLELLDLG
YNRIRSLARNVFAGMIRLKEHLEHNQFSKLNALFPRLVSLQONLYLQWNKISVIGQTMSWTW
SSLQRLDLSGNEIEAFSGPSVFQCPNLQRLNLDLSNKLTFIGQEILDSWISLNDISLAGNIWE
CSRNICSLVNWLKSFKGLRENTIICASPKELOGVNVIDAVKNYSICGKSTTERFDLARALPKP
TFKPKLPRPKHESKPPLPPTVGATEPGPETDADAEHISFHKIIAGSVALFLSVLVILLVIYVS
WKRYPASMQLQQRSLMRRHRKKKRQSLKQMT PSTQEFYVDYKPTNTETSEMLLNGTGPCTYN
KSGSRECEV

Important features:**Signal peptide:**

amino acids 1-33

Transmembrane domain:

amino acids 420-442

N-glycosylation sites.

amino acids 126-129, 357-360, 496-499, 504-507

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 465-468

Tyrosine kinase phosphorylation site.

amino acids 136-142

N-myristoylation sites.

amino acids 11-16, 33-38, 245-250, 332-337, 497-502, 507-512

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FIGURE 537

GGGACTACAAGCCGCGCCGCGCTGCCGCTGGCCCCCTCAGCAACCCTCGAC**ATG**GCGCTGAGGCGGCCACCGCGAC
TCCGGCTCTGCGCTCGGCTGCCTGACTTCTTCCTGCTGCTGCTTTTCAGGGGCTGCCTGATAGGGGCTGTAAATC
TCAAATCCAGCAATCGAACCCAGTGGTACAGGAATTTGAAAGTGTGGAAGTGTCTTGCATCATTACGGATTTCGC
AGACAAGTGACCCAGGATCGAGTGAAGAAAATTTCAAGATGAACAAACCACATATGTGTTTTTTGACAACAAAA
TTCAGGGAGACTTGGCGGGTCGTGCAGAAATACTGGGGAAGACATCCCTGAAGATCTGGAATGTGACACGGAGAG
ACTCAGCCCTTTATCGCTGTGAGGTGCTTGTCTCGAAATGACCGCAAGGAAATTTGATGAGATTGTGATCGAGTTAA
CTGTGCAAGTGAAGCCAGTGACCCCTGTCTGTAGAGTGCCGAAGGCTGTACCAGTAGGCAAGATGGCAACACTGC
ACTGCCAGAGAGTGTAGGGCCACCCCGGCCCTCATACTAGCTGGTATCGCAATGATGTACCACTGCCACGGATT
CCAGAGCCAATCCAGATTTTCGCAATTTCTTTTCCACTTAAACTCTGAAACAGGCACCTTTGGTGTTCAGTGTCTG
TTCACAAGGACGACTCTGGGCAGTACTACTGCATTGCTTCCAATGACGCAGGCTCAGCCAGGTGTGAGGAGCAGG
AGATGGAAGTCTATGACCTGAACATTGGCGGAATTATTGGGGGGGTTCTGGTTGTCTTGTCTGACTGGCCCTGA
TCACGTTGGGCATCTGCTGTGCATACAGACGTGGCTACTTCATCAACAATAAACAGGATGGAGAAAAGTTACAAGA
ACCCAGGGAAACCAGATGGAGTTAACTACATCCGCACTGACGAGGAGGGCGACTTCAGACACAAGTCATCGTTTTG
TGATCT**TGA**GACCCGCGGTGTGGCTGAGAGCGCAGAGCGCACGTGCACATACCTCTGTAGAAAATCCTGTCAA
GGCAGCGAGAGTGTGACCTCGGACAGAGCTAGACACTCATTCAGAAGCTTTTCGTTTTGGCCAAAAGTTGACCA
CTACTCTTCTTACTCTAACAAGCCACATGAATAGAAGAATTTTCCTCAAGATGGACCCGGTAAATATAACCACAA
GGAAGCGAAACTGGGTGCGTTCACTGAGTTGGGTTCCCTAATCTGTTTTCTGGCCTGATTCCCGCATGAGTATTAGG
GTGATCTTAAAGAGTTTGCTCACGTAAACGCCCGTGTGGGCCCTGTGAAGCCAGCATGTTCAACCACTGGTCTGTT
CAGCAGCCACGACAGCACCATGTGAGATGGCGAGGTGGCTGGACAGCACCAGCAGCGCATCCCGGCGGGAACCCA
GAAAAGGCTTCTTACACAGCAGCCTTACTTCATCGCCCCAGACACCACCGCAGTTTCTTAAAGGCTCTGC
TGATCGGTGTTGCAGTGTCCATTGTGGAGAAGCTTTTGGATCAGCATTTTGTAAAAACAACCAAAATCAGGAAG
GTAAATTGGTTGCTGGAAGAGGGATCTTGCCTGAGGAACCCTGCTTGTCCAACAGGGTGTGAGGATTTAAGGAAA
ACCTTCGTCTTAGGCTAAGTCTGAAATGGTACTGAAATATGCTTTTCTATGGGTCTTGTTTATTTTATAAAATTT
TACATCTAAATTTTGTCTAAGGATGTATTTTGATTATTGAAAAAGAAAATTTCTATTTAACTGTAAATATATTGT
CATACAATGTTAAATAACCTATTTTTTTTAAAAAAGTTCAACTTAAGGTAGAAGTTCCAAGCTACTAGTGTTAAAT
TGGAATAATCAATAATTAAGAGTATTTTACCCAAGGAATCCTCTCATGGAAGTTTACTGTGATGTTCTTTTCT
CACACAAGTTTGTAGCTTTTTCACAAGGGAACCTACTGTCTACACATCAGACCATAGTTGCTTAGGAAACCTT
TAAAAATTCAGTTAAGCAATGTTGAAATCAGTTTGCATCTCTTCAAAAGAAACCTCTCAGGTTAGCTTTGAACT
GCCTCTTCTGAGATGACTAGGACAGTCTGTACCCAGAGGCCACCCAGAAGCCCTCAGATGTACATACACAGATG
CCAGTCAGCTCCTGGGGTTGCGCCAGGCGCCCCCGCTCTAGCTCACTGTTGCCTCGCTGTCTGCCAGGAGGCCCT
GCCATCCTTGGGCCCTGGCAGTGGCTGTGTCCAGTGAGCTTACTCACGTGGCCCTTGCTTCATCCAGCACAGC
TCTCAGGTGGGCACTGCAGGGACACTGGTGTCTTCCATGTAGCGTCCAGCTTTGGGCTCCTGTAACAGACCTCT
TTTTGGTTATGGATGGCTCACAAAATAGGGCCCCCAATGCTATTTTTTTTTTTTAAAGTTTGTAAATATTTGTT
AAGATTGTCTAAGGCCAAAGGCAATTGCGAAATCAAGTCTGTCAAGTACAATAACATTTTTTAAAGAAAAATGGAT
CCCACTGTTCTTGTCCACAGAGAAAGCACCCAGACGCCACAGGCTCTGTGCGATTTCAAACAAACCATGAT
GGAGTGGCGGCCAGTCCAGCCTTTTAAAGAACGTGAGGTGGAGCAGCCAGGTGAAAGGCCTGGCGGGGAGGAAAG
TGAACGCCTGAATCAAAAGCAGTTTTCTAATTTTGACTTTAAATTTTTTATCCGCCGGAGACACTGCTCCCAT
TGTGGGGGGACATTAGCAACATCACTCAGAAGCCTGTGTTCTTCAAGAGCAGGTGTTCTCAGCCTCACATGCCCT
GCCGTGCTGGACTCAGGACTGAAGTGTGTAAAGCAAGGAGCTGCTGAGAAGGAGCACTCCACTGTGTGCTGGA
GAATGGCTCTCACTACTCACCTTGTCTTTTCACTTCCAGTGTCTTGGGTTTTTTTATACTTTGACAGCTTTTTTTT
AATTGCATACATGAGACTGTGTTGACTTTTTTTTAGTTATGTGAAACACTTTTGCCGAGGCCGCTGGCAGAGGCA
GGAAATGCTCCAGCAGTGGCTCAGTGTCTCCCTGGTGTCTGCTGCATGGCATCCTGGATGCTTAGCATGCAAGTTC
CTCCATCATTTGCCACCTTGGTAGAGAGGGATGGCTCCCCACCTCAGCGTTGGGGATTACGCTCCAGCCTCCT
TCTTGGTTGTCATAGTGATAGGGTAGCCTTATTGCCCCCTCTTCTTATACCCTAAAACCTTCTACACTAGTGCCA
TGGGAACCAGGTCTGAAAAAGTAGAGAGAAGTGAAGTAGAGTCTGGGAAGTAGCTGCCTATAACTGAGACTAGA
CGGAAAAGGAATACTCGTGTATTTTAAAGATATGAATGTGACTCAAGACTCGAGGCCGATACAGGCTGTGATTCT
GCCTTTGGATGGATGTTGCTGTACACAGATGCTACAGACTTGTACTAACACACCGTAATTTGGCATTTGTTTAAAC
CTCATTTATAAAAGCTTCAAAAAAACCCA

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FIGURE 538

MALRRPPRLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQTS DP
RIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTS LKIWNVTRRDSALYRCEVVARNDRKEI
DEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPLPTDSRANPR
FRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVDNLNIGGIIGGVLVV
LAVLALITLGICCA YRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEGDFRHKSSFVI

Important features:**Signal peptide:**

amino acids 1-30

Transmembrane domain:

amino acids 243-263

N-glycosylation sites.

amino acids 104-107, 192-195

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 107-110

Casein kinase II phosphorylation site.

amino acids 106-109, 296-299

Tyrosine kinase phosphorylation site.

amino acids 69-77

N-myristoylation sites.

amino acids 26-31, 215-220, 226-231, 243-248, 244-249, 262-267

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FIGURE 539

CCAGGACCAGGGCGCACCGGCTCAGCCTCTCACTTGTCAGAGGCCGGGGAAGAGAAGCAAAGC
GCAACGGTGTGGTCCAAGCCGGGGCTTCTGCTTCGCTCTAGGACATACACGGGACCCCTAA
CTTCAGTCCCCCAAACGCGCACCCCTCGAAGTCTTGAAGTCCAGCCCCGCACATCCACGCGCGG
CACAGGCGCGGCAGGCGGCAGGTCCCGGCCGAAGGCGATGCGCGCAGGGGGTTCGGGCAGCTGG
GCTCGGGCGGGCGGGAGTAGGGCCCCGGCAGGGAGGCAGGGAGGCTGCATATTCAGAGTCGCGGG
CTGCGCCCTGGGCAGAGGCCGCCCTCGCTCCACGCAACACCTGCTGCTGCCACCGCGCCGCGGA
TGAGCCGCGTGGTCTCGCTGCTGCTGGGCGCCGCGCTGCTCTGCGGCCACGGAGCCTTCTGCC
GCCGCGTGGTCAGCGGCCAAAAGGTGTGTTTTGCTGACTTCAAGCATCCCTGCTACAAAATGG
CCTACTTCCATGAACTGTCCAGCCGAGTGAGCTTTTCAAGGAGGCACGCCTGGCTTGTGAGAGTG
AGGGAGGAGTCTCCTCAGCCTTGAGAATGAAGCAGAACAGAAGTTAATAGAGAGCATGTTGC
AAAACCTGACAAAACCCGGGACAGGGATTTCTGATGGTGATTTCTGGATAGGGCTTTGGAGGA
ATGGAGATGGGCAAACATCTGGTGCCTGCCAGATCTCTACCAGTGGTCTGATGGAAGCAATT
CCCAGTACCGAAACTGGTACACAGATGAACCTTCCTGCGGAAGTGAAAAGTGTGTTGTGATGT
ATCACCAACCAACTGCCAATCCTGGCCTTGGGGGTCCCTACCTTTACCAGTGGAATGATGACA
GGTGTAAACATGAAGCACAATTATATTTGCAAGTATGAACCAGAGATTAATCCAACAGCCCCCTG
TAGAAAAGCCTTATCTTACAAATCAACCAGGAGACACCCATCAGAATGTGGTTGTTACTGAAG
CAGGTATAATTCCCAATCTAATTTATGTTGTTATACCAACAATACCCCTGCTCTTACTGATAC
TGTTTGCTTTTGGAACTGTGTTTCCAGATGCTGCATAAAAGTAAAGGAAGAACAAAAACTA
GTCCAAACCAGTCTACACTGTGGATTTCAAAGAGTACCAGAAAAGAAAGTGGCATGGAAGT**AT**
AATAAGTCAATTGACTTGGTTCAGAAATTTTGTAATTCTGGATCTGTATAAGGAATGGCATCAG
AACAAATAGCTTGAATGGCTTGAAATCACAAAGGATCTGCAAGATGAACTGTAAGCTCCCCCT
TGAGGCAAATATTAAGTAATTTTTATATGTCTATTATTTTCAATTTAAAGAATATGCTGTGCTA
ATAATGGAGTGAGACATGCTTATTTTGCTAAAGGATGCACCCAACTTCAAACCTTCAAGCAAA
TGAAATGGACAATGCAGATAAAGTTGTTATCAACACGTCGGGAGTATGTGTGTTAGAAGCAAT
TCCTTTTATTTCTTTTACCTTTTCATAAGTTGTTATCTAGTCAATGTAATGTATATTGTATTGA
AATTTACAGTGTGCAAAAGTATTTTACCTTTGCATAAGTGTGTTGATAAAAATGAACTGTTCTA
ATATTTATTTTTATGGCATCTCATTTTTTCAATACATGCTCTTTTGATTAAAGAACTTATTAC
TGTTGTCAACTGAATTCACACACACACAAATATAGTACCATAGAAAAAGTTTGTGTTTCTCGAA
ATAATTCATCTTTCAGCTTCTCTGCTTTTGGTCAATGTCTAGGAAATCTCTTCAGAAATAAGA
AGCTATTTTCAATTAAGTGTGATATAAACCTCCTCAAACATTTTACTTAGAGGCAAGGATTGTCT
AATTTCAATTGTGCAAGACATGTGCCTTATAATTATTTTTTAGCTTAAATTAACAGATTTTG
TAATAATGTAACTTTGTTAATAGGTGCATAAACACTAATGCAGTCAATTTGAACAAAAGAAGT
GACATACACAATATAAATCATATGTCTTCACACGTTGCCTATATAATGAGAAGCAGCTCTCTG
AGGGTTCTGAAATCAATGTGGTCCCTCTCTTGCCCACTAAACAAAGATGGTTGTTTCGGGGTTT
GGGATTGACACTGGAGGCAGATAGTTGCAAAGTTAGTCTAAGGTTTCCCTAGCTGTATTTAGC
CTCTGACTATATTAGTATACAAAGAGGTCATGTGGTTGAGACCAGGTGAATAGTCACTATCAG
TGTGGAGACAAGCACAGCACACAGACATTTTAGGAAGGAAAGGAACACTACGAAATCGTGTGAAA
ATGGGTTGGAACCCATCAGTGATCGCATATTCATTGATGAGGGTTTGCTTGAGATAGAAAATG
GTGGCTCCTTTCTGTCTTATCTCCTAGTTTCTTCAATGCTTACGCCTTGTTCTTCTCAAGAGA
AAGTTGTAAGTCTCTGGTCTTCATATGTCCCTGTGCTCCTTTTAACCAATAAAGAGTTCTTG
TTTCTGGGGGAAA

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FIGURE 540

MSRVVSLLLGAALLCGHGAFRRVVSQGKVCFADFKHPCYKMAYFHELSSRVSFQEARLACES
EGGVLLSLENEAEQKLIESMLQNLTKPGTGISDGDWIGLWRNGDGQTSGACPDLYQWSDGSN
SQYRNWYTDEPSCGSEKCVVMYHQPTANPGLGGPYLYQWNDDRCNMKHNYICKYEPEINPTAP
VEKPYLTNQPGDTHQNVVVTEAGIIPNLIYVVIPTIPLLLLILVAFGTCCFQMLHKSKGRKT
SPNQSTLWISKSTRKESGMEV

Important features:**Signal peptide:**

amino acids 1-21

Transmembrane domain:

amino acids 214-235

N-glycosylation sites.

amino acids 86-89 and 255-258

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 266-269

N-myristoylation sites.amino acids 27-32, 66-71, 91-96, 93-98, 102-107, 109-114, 140-145
and 212-217

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FIGURE 541

GGAGAA**ATG**GAGAGAGCAGTGAGAGTGGAGTCCGGGGTCTGGTCCGGGGTGGTCTGTCTGCTCCTGGCATGCCCTG
 CCACAGCCACTGGGGCCGAAGTTGCTCAGCCTGAAGTAGACACCACCCTGGGTGCTGTGCGAGGGCCGGCAGGTGG
 GCGTGAAGGGCACAGACCGCCTTGTGAATGTCTTTCTGGGGCATTCATTTGCCAGCCGCCACTGGGGCCCTGACC
 GGTTCTCAGCCCCACACCCAGCACAGCCCTGGGAGGGTGTGCGGGATGCCAGCACTGCGCCCCCAATGTGCCTAC
 AAGACGTGGAGAGCATGAACAGCAGCAGATTTGTCTCAACGGAACAGCAGATCTTCTCCGTTCAGAGGACT
 GCCTGGTCTCAACGTCTATAGCCAGCTGAGGTCCCCGCAGGGTCCGGTAGGCCGGTTCATGGTATGGGTCCATG
 GAGGCGCTCTGATAACTGGCGCTGCCACCTCCTACGATGGATCAGCTCTGGCTGCCTATGGGGATGTGGTCTGTG
 TTACAGTCCAGTACCGCCTTGGGGTCTTGGCTTCTTCAGCACTGGAGATGAGCATGCACCTGGCAACCAGGGCT
 TCCTAGATGTGGTAGCTGCTTTGCGCTGGGTGCAAGAAACATCGCCCCCTTCGGGGGTGACCTCAACTGTGTCA
 CTGTCTTTGGTGGATCTGCCGGTGGGAGCATCATCTCTGGCCTGGTCTGTCCCCAGTGGCTGCAGGGCTGTTCC
 ACAGAGCCATCACACAGAGTGGGGTTCATCACCACCCAGGGATCATCGACTCTCACCCTTGGCCCCCTAGCTCAGA
 AAATCGCAAACACCTTGGCCTGCAGCTCCAGCTCCCCGGCTGAGATGGTGCAGTGCCTTCAGCAGAAAGAAGGAG
 AAGAGCTGGTCTTAGCAAGAAGCTGAAAAATACTATCTATCCTCTCACCCTTGATGGCACTGTCTTCCCCAAAA
 GCCCCAAGGAACTCCTGAAGGAGAAGCCCTTCCAGAGCTGTGCCCTTCCCTCATGGGTGTCAACAACCATGAGTTCA
 GCTGGCTCATCCCCAGGGGTGGGGTCTCCTGGATACAATGGAGCAGATGAGCCGGGAGGACATGCTGGCCATCT
 CAACACCCGTCTTGACCAGTCTGGATGTGCCCCCTGAGATGATGCCACCGTCATAGATGAATACCTAGGAAGCA
 ACTCGGACGCACAAGCCAAATGCCAGGCGTTCCAGGAATTCATGGGTGACGTATTCATCAATGTTCCCACCGTCA
 GTTTTTCAAGATACCTTCGAGATTCTGGAAGCCCTGTCTTTTCTATGAGTTCCAGCATCGACCCAGTTCTTTTG
 CGAAGATCAAACCTGCCTGGGTGAAGGCTGATCATGGGGCCGAGGGTGCTTTTGTGTTCCGAGGTCCCTTCCTCA
 TGGACGAGAGCTCCCGCCTGGCCTTTCAGAGGCCACAGAGGAGAGAAGCAGCTAAGCCTCACCATGATGGCCC
 AGTGGACCCACTTTGCCCGGACAGGGGACCCCAATAGCAAGGCTCTGCCTCCTTGGCCCCAATTCAACCAGGCGG
 AACAATATCTGGAGATCAACCCAGTGCCACGGGCCGGACAGAAGTTCAGGGAGGCCTGGATGCAGTTCTGGTCAG
 AGACGCTCCCCAGCAAGATACAACAGTGGCACCAGAAGCAGAAGAAGCAGGAAGGCCAGGAGGACCTCT**GA**AGGCC
 AGGCCTGAACCTTCTTGGCTGGGGCAAACCACTCTTCAAGTGGTGGCAGAGTCCCAGCACGGCAGCCCCGCCTCTC
 CCCCTGCTGAGACTTTAATCTCCACAGCCCTTAAAGTGTGCGCCGCTCTGTGACTGGAGTTATGCTCTTTTGAA
 ATGTCAACAAGGCCGCTCCACCTCTGGGGCATTGTACAAGTTCTTCCCTCTCCCTGAAGTGCTTCTCCTGCTTT
 CTTGCTGCTAGGTTCTAGCACATTCTCTAGCTTCTTGGAGGACTCACTCCCCAGGAAGCCTTCCCTGCCTTCTC
 TGGGCTGTGCGGCCCCGAGTCTGCGTCCATTAGAGCACAGTCCACCCAGGCTAGCACCGTGTCTGTGTCTGTCT
 CCCCCCTCAGAGGAGCTCTCTCAAATGGGGATTAGCCTAACCCACTCTGTACCCACACCAGGATCGGGTGGGA
 CCTGGAGCTAGGGGGTGTGTTGCTGAGTGAGTGAGTGAAACACAGAATATGGGAATGGCAGCTGCTGAACCTGAAC
 CCAGAGCCTTCAGGTGCCAAAGCCATACTCAGGCCCCCACCAGCATTGTCCACCCTGGCCAGAAGGGTGCATGCC
 AATGGCAGAGACCTGGGATGGGAGAAGTCTTGGGGCAGGAGGATCCAGCCTAGAGCAGACCTTAGCCCTTGAC
 TAAGGCCCTCAGACTAGGGCGGGAGGGGTCTCCTCCTCTCTGCTGCCAGTCTTGGCCCCCTGCACAAGACAACAGA
 ATCCATCAGGGCCATGAGTGTACCCAGACCTGACCCTCACCAATTCCAGCCCCCTGACCCTCAGGACGCTGGATG
 CCAGCTCCCAGCCCCAGTGCCGGGTCTCCTCCTCCTTCTGGCTTGGGGAGACCAGTTTCTGGGGAGCTTCCAAG
 AGCACCCACCAAGACACAGCAGGACAGGCCAGGGGAGGGCATCTGGACCAGGGCATCCGTCGGGCTATTGTACACA
 GAGAAAAGAAGAGACCCACCCACTCGGGCTGCAAAAGGTGAAAAGCACCAAGAGGTTTTTCAGATGGAAGTGAGAG
 GTGACAGTGTGCTGGCAGCCCTCACAGCCCTCGCTTGCTCTCCCTGCGCCTCTGCCTGGGGTCCCACTTTGGCA
 GCACTTGAGGAGCCCTTCAACCCGCGCTGCACTGTAGGAGCCCTTCTGCGGCTGGCCAAGGCCGAGCCAGCT
 CCCTCAGCTTGCGGGGAGGTGCGGAGGGAGAGGGGCGGGCAGGAACCGGGGCTGCGCGCAGCGCTTGCGGGCCAG
 AGTGAGTTCCGGGTGGGCGTGGGCTCGGCGGGGCCCCACTCAGAGCAGCTGGCCGGCCCCAGGCAGTGAGGGCCT
 TAGCACCTGGGCCAGCAGCTGCTGTGCTCGATTTCTCGCTGGGCCCTTAGCTGCCTCCCCGCGGGGAGGGCTCGG
 GACCTGCAGCCCTCCATGCCTGACCCTCCCCCACCCTCGTGGGCTCCTGTGCGGCGGAGCCTCCCCAAGGAG
 CGCCGCCCCCTGCTCCACAGCGCCAGTCCCATCGACCACCCAAAGGGCTGAGGAGTGCGGGTGACAGCGCGGGA
 CTGGCAGGCAGCTCCACCTGCTGCCCCAGTGTGGATCCACTGGGTGAAGCCAGCTGGGCTCCTGAGTCTGGTGG
 GGACTTGAGAAACCTTTATGTCTAGCTAAGGGATTGTAAATACACCGATGGGCACTCTGTATCTAGCTCAAGGTT
 TGTAACACACCAATCAGCACCTGTGTCTAGCTCAGTGTGTTGTGAATGCACCAATCCACACTCTGTATCTGGCT
 ACTCTGGTGGGGACTTGGAGAACCTTTGTGTCCACACTCTGTATCTAGCTAATCTAGTGGGGATGTGGAGAACCT
 TTGTGTCTAGCTCAGGGATCGTAAACGCACCAATCAGCACCTGTCAAACAGACCACTGACTCTCTGTAAAAAT
 GGACCAATCAGCAGGATGTGGGTGGGGCAGACAAGAAATAAAAGCAGGCTGCCTGAGCCAGCATGACAACCC
 CCCTCGGGTCCCCTCCCACGCCGTGGAAGCTTTGTTCTTTTCGCTCTTTGCAATAAATCTTGCTACTGCCCAAAA

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FIGURE 542

MERAVRVESGVLVGVVCLLLACPATATGPEVAQPEVDTTLGRVVRGRQVGKGTDRLVNVFLGI
PFAQPPLGPDREFSAPHPAQFWEQVRDASTAPPMCLQDVESMNSSRFVLNGKQQIFSVSEDCLV
LNVYSPAIEVPAGSGRPVMVWVHGGALITGAATSYDGSALAAAGDVVVVTVQYRLGVLGFFSTG
DEHAPGNQGFLLDVVAALRWVQENIAPFGGDLNCVTVFGGSSAGGSIISGLVLS PVAAGLFHRAI
TQSGVITTPGIIDSHPWPLAQKIAN TLACSSSSPAEMVQCLQQKEGEELVLSKKLKNTIYPLT
VDGTVFVPKSPKELLKEKPFHSVPFLMGVNNHEFSWLI PRGWGLLDTMEQMSREDMLAISTPVL
TSLDVPPPEMMPTVIDEYLG SNSDAQAKCQAFQEFMGDVFINVPTVSFSRYLRDSGSPVFFYEF
QHRPSSF AKIKPAWVKADHGAEGAFVFGGPFLMDESSRLAFPEATEEEKQLSLTMM AQWTHFA
RTGDPNSKALPPWPQFNQAEQYLEINPVPRAGQKFREAWMQFWSETLPSKIQQWHQKQKNRKA
QEDL

Important features:**Signal peptide:**

amino acids 1-27

Transmembrane domain:

amino acids 226-245

N-glycosylation site.

amino acids 105-109

N-myristoylation sites.

amino acids 10-16, 49-55, 62-68, 86-92, 150-156, 155-161,
162-168, 217-223, 227-233, 228-234, 232-238, 262-268, 357-363,
461-467

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 12-23

Carboxylesterases type-B serine active site.

amino acids 216-232

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FIGURE 543

TGTCGCCTGGCCCTCGCC**ATG**CAGACCCCGGAGCGTCCCCTCCCCGCCCGGCCCTCCTGCTTCTGCTGCTGCTA
CTGGGGGGCGCCACGGCCTCTTTCTGAGGAGCCGCCCGCTTAGCGTGGCCCCCAGGGACTACCTGAACCAC
TATCCCGTGTTTGTGGGCAGCGGGCCCGGACGCCTGACCCCGCAGAAGGTGCTGACGACCTCAACATCCAGCGA
GTCCTGCGGGTCAACAGGACGCTGTTCAATTGGGGACAGGGACAACCTCTACCGCGTAGAGCTGGAGCCCCCAGC
TCCACGGAGCTGCGGTACCAGAGGAAGCTGACCTGGAGATCTAACCCAGCGACATAAACGTGTGTGCGATGAAG
GGCAAACAGGAGGGCGAGTGTGCGAACTTCGTAAAGGTGCTGCTCCTTCGGGACGAGTCCACGCTCTTTGTGTGC
GGTTCCAACGCCTTCAACCCGGTGTGCGCAACTACAGCATAGACACCCTGCAGCCCGTCGGAGACAACATCAGC
GGTATGGCCCGCTGCCCCTACGACCCCAAGCAGCCCAATGTTGCCCTCTTCTCTGACGGGATGCTCTTCACAGCT
ACTGTTACCGACTTCCTAGCCATTGATGCTGTGCTCATCTACCGCAGCCTCGGGACAGGCCCCACCTGCGCACCGTG
AAACATGACTCCAAGTGGTTCAAGAGCCTTACTTTGTCCATGCGGTGGAGTGGGGCAGCCATGTCTACTTCTTC
TTCCGGGAGATTGCGATGGAGTTTAACTACCTGGAGAAGGTGGTGGTGTCCCGCTGGCCCCAGTGTGCAAGAAC
GACGTGGGAGGCTCCCCCGCGTGCTGGAGAAGCAGTGGACGTCCTTCCTGAAGGCGCGGCTCAACTGCTCTGTA
CCCGGAGACTCCCATTTCTACTTCAACGTGCTGCAGGCTGTACGGGCGTGGTCAGCCTCGGGGGCCGGCCCGTG
GTCCTGGCCGTTTTTTCCACGCCCAGCAACAGCATCCCTGGCTGGCTGTCTGCGCCTTTGACCTGACACAGGTG
GCAGCTGTGTTTGAAGGCCGCTTCCGAGAGCAGAAGTCCCCGAGTCCATCTGGACGCGGTTGCCGGAGGATCAG
GTGCCTCGACCCCGGCCCGGGTGTGCGCAGCCCCCGGGATGCAGTACAATGCCTCCAGCGCCTTGCCGGATGAC
ATCCTCAACTTTGTCAAGACCCACCCTCTGATGGACGAGGCGGTGCCCTCGCTGGGCCATGCGCCCTGGATCCTG
CGGACCCTGATGAGGCACACGCTGACTCGAGTGGCTGTGGACGTGGGAGCCGGCCCCCTGGGGCAACCAGACCGTT
GTCTTCCTGGGTCTGAGGCGGGGACGGTCCTCAAGTTCCTCGTCCGGCCCAATGCCAGCACCTCAGGGACGTCT
GGGCTCAGTGTCTTCTTGAGGAGTTTGAGACCTACCGGCCGGACAGGTGTGGACGGCCCGGCTGGCGAGACA
GGGCAGCGGCTGCTGAGCTTGGAGCTGGACGCAGCTTCGGGGGGCCTGCTGGCTGCCTTCCCCCGCTGCGTGGTC
CGAGTGCCTGTGGCTCGCTGCCAGCAGTACTCGGGGTGTATGAAGAACTGTATCGGCAGTCAGGACCCCTACTGC
GGGTGGGGCCCCGACGGCTCCTGCATCTTCTCAGCCCCGGGCACCAGAGCCGCCTTTGAGCAGGACGTGTCCGGG
GCCAGCACCTCAGGCTTAGGGGACTGCACAGGACTCCTGCGGGCCAGCCTCTCCGAGGACCGCGCGGGGCTGGTG
TCGGTGAACCTGCTGGTAACGTCGTCGGTGGCGGCCCTTCGTGGTGGGAGCCGTGGTGTCCGGCTTCAGCGTGGGC
TGGTTCGTGGGCCTCCGTGAGCGGGCGGAGCTGGCCCGCGCAAGGACAAGGAGGCCATCCTGCGCGACGGGGCG
GGCGAGGCGGTGCTGAGCGTCAGCCGCTGGGCGAGCGCAGGGCGCAGGGTCCCGGGGGCCGGGGCGGAGGCGGT
GGCGGTGGCGCCGGGGTTCCCCCGAGGGCCTGCTGGCGCCCCTGATGCAGAACGGCTGGGCCAAGGCCACGCTG
CTGCAGGGCGGGCCCCACGACCTGGACTCGGGGTGCTGCCCCACGCCGAGCAGACGCCGCTGCCGCGAAGCGC
CTGCCCCACTCCGCACCCGCACCCCCACGCCCTGGGCCCCCGCGCCTGGGACCACGGCCACCCCCCTGCTCCCGGCC
TCCGCTTCATCCTCCTCCTGCTGCTGGCGCCCGCGGGCCCCCGAGCAGCCCCCGCGCCTGGGGAGCCGACC
CCCGAGCCCGCCTTATGCTGCCCGGCCCGGCCGCGCTCCACGCGGACTTCCCGCTCACCCCCACGCGAGC
CCGGACCGCCGGCGGGTGGTGTCCGCGCCACGGGCCCTTGGACCAGCCTCAGCCGCCGATGGCCTCCCGCGG
CCCTGGAGCCCCGCCCCGACGGGCAGCCTGAGGAGGCCACTGGGCCCCACGCCCTCCGGCCGCCACCCTGCGC
CGCACCCACACGTTCAACAGCGGCGAGGCCCGGCCTGGGGACCGCCACCGCGGCTGCCACGCCCGGCCGGGCACA
GACTTGGCCACCTCCTCCCCATGTTTTGGGGGGCGGACAGGACTGCGCCCCCGTGCCCT**TAGG**CGGGGGGGCCCCCG
ATGCCTTGGCAGTGCCAGCCACGGGAACCAGGAGCGAGAGACGGTGCCAGAACGCCGGGGCCCGGGGCAACTCCG
AGTGGGTGCTCAAGTCCCCCGCGACCCACCCGCGGAGTGGGGGGCCCCCTCCGCCACAAGGAAGCACAAACCAG
CTCGCCCTCCCCCTACCCGGGGCCGCGAGGACGCTGAGACGGTTTGGGGGTGGGTGGGCGGGAGGACTTTGCTATG
GATTTGAGGTTGACCTTATGCGCGTAGGTTTTGGTTTTTTTTTGCAGTTTTGGTTTTCTTTTGGGTTTTCTAACC
AATTGCACAACCTCCGTTCTCGGGGTGGCGGCAGGCAGGGGAGGCTTGACGCGCGGTGGGGAATGGGGGGCCACAG
CTGCAGACCTAAGCCCTCCCCCACCCTGGAAAGGTCCCTCCCCAACCCAGGCCCTGGCGTGTGTGGGTGTGCG
TGCGTGTGCGTGCCGTGTTCTGTGTGCAAGGGGCGGGGAGGTGGGCGTGTGTGTGCGTGCCAGCGAAGGCTGCTG
TGGGCGTGTGTGTAAGTGGGCCACGCGTGCAAGGTGTGTGTCCACGAGCGACGATCGTGGTGGCCCCAGCGGCC
TGGGCGTTGGCTGAGCCGACGCTGGGGCTTCCAGAAGGCCCGGGGTCTCCGAGGTGCCGGTTAGGAGTTTGAAC
CCCCCCTCTGCGAGAGGGAAGCGGGGACAATGCCGGGTTTCAGGCAGGAGACACGAGGAGGGCCTGCCCGGA
AGTCACATCGGCAGCAGCTGTCTAAAGGGCTTGGGGGCTGGGGGGCGGCGAAGGTGGGTGGGGCCCCCTCTGTAA
ATACGGCCCCAGGGTGGTGAGAGAGTCCCATGCCACCCGTCCCTTGTGACCTCCCCCTATGACCTCCAGCTGA
CCATGCATGCCACGTGGCTGGCTGGGTCTCTGCCCTCTTTGGAGTTTGCCTCCCCCAGCCCCCTCCCCATCAAT
AAAACCTCTGTTTACAACCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

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FIGURE 544

MQTPRASPPRPALLLLLLLLGGAHGLFPEEPPLSVAPRDYLNHYPVFVGSGPGRLTPAEGAD
DLNIQRLVRVNRTLFIGDRDNLYRVELEPPTSTELRYQRKLTWRSNPSDINVCRMKGKQEGEC
RNFVKVLLLRDESTLFVCGSNAFNPVCANYSIDTLQPVGDNISGMARCPYDPKHANVALFSDG
MLFTATVTDFLAIDAVIYRSLGDRPTLRTVKHDSKWFKEPYFVHAVEWGS HVYFFFREIAMEF
NYLEKVVVSRVARVCKNDVGGSPRVLEKQWTSFLKARLNC SVPGDSHFYFNVLQAVTG VVSLG
GRPVVLAVFSTPSNSIPGS AVCAFDLTQVA AVFEGRFREQKSPESI WTPVPEDQVPRPRPGCC
AAPGMQYNASSALPDDILNFVKTHPLMDEAVPSLGHAPWILRTLMRHQLTRVAVDVGAGPWGN
QTVVFLGSEAGTVLKFLVRPNASTSGTSGLSVFLEEFETYR PDRCGRPGGETGQRLLSLELD
AASGGLLA AFPRCVVRVPVARCQQYSGCMKNCIGSQDPYCGWAPDGSCIFLSPGTRAAFEQDV
SGASTSGLGDCTGLLRASLSEDRAGLVSVNLLVTSSVAAFVVGAVVSGFSVGFVGLRERREL
ARRKDKEAILAHGAGEAVLSVSRLGERRAQGPGGGGGGGGGAGVPPEALLAPLMQNGWAKAT
LLQGGPHDLDSGLLPTPEQTPLPQKRLPTPHPHPHALGPRAWDHGHPLLPASASSSLLLLAPA
RAPEQPPAPGEPTPDGRLYAARPGRASHGDFLTPHASPDRRRVVSAPTGPLDPASAADGLPR
PWSPPPTGSLRRPLGPHAPPAATLRRTHTFNSGEARPGDRHRGCHARPGTDLAHL LPPYGGADR
TAPPVP

Important features:**Signal peptide:**

amino acids 1-25

Transmembrane domains:

amino acids 318-339, 598-617

N-glycosylation sites.amino acids 74-78, 155-159, 167-171, 291-295, 386-390, 441-445,
462-466**Glycosaminoglycan attachment sites.**

amino acids 51-55, 573-577

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 102-106

N-myristoylation sites.amino acids 21-27, 50-56, 189-195, 333-339, 382-388, 448-454,
490-496, 491-497, 508-514, 509-515, 531-537, 558-564, 569-575,
574-580, 580-586, 610-616, 643-649, 663-669, 666-672, 667-673,
668-674, 669-675, 670-676, 868-874, 879-885

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FIGURE 545

GATGGCGCAGCCACAGCTTCTGTGAGATTTCGATTTCTCCCCAGTTCCCCTGTGGGTCTGAGGG
GACCAGAAGGGTGAGCTACGTTGGCTTTCTGGAAGGGGAGGCTAT**ATG**CGTCAATTCCCCAAA
ACAAGTTTTGACATTTCCCCTGAAATGTCATTCTCTATCTATTCACTGCAAGTGCCTGCTGTT
CCAGGCCTTACCTGCTGGGCACTAACGGCGGAGCCAGGATGGGGACAGAATAAAGGAGCCACG
ACCTGTGCCACCAACTCGCACTCAGACTCTGAACTCAGACCTGAAATCTTCTCTTCACGGGAG
GCTTGGCAGTTTTTCTTACTCCTGTGGTCTCCAGATTTCAGGCCTAAGATGAAAGCCTCTAGT
CTTGCCCTTCAGCCTTCTCTCTGCTGCGTTTTATCTCCTATGGACTCCTTCCACTGGACTGAAG
ACACTCAATTTGGGAAGCTGTGTGATCGCCACAAACCTTCAGGAAATACGAAATGGATTTTCT
GAGATACGGGGCAGTGTGCAAGCCAAAGATGGAAACATTGACATCAGAATCTTAAGGAGGACT
GAGTCTTTGCAAGACACAAAGCCTGCGAATCGATGCTGCCTCCTGCGCCATTTGCTAAGACTC
TATCTGGACAGGGTATTTAAAACTACCAGACCCCTGACCATTATACTCTCCGGAAGATCAGC
AGCCTCGCCAATTCCTTTCTTACCATCAAGAAGGACCTCCGGCTCTCTCATGCCACATGACA
TGCCATTGTGGGGAGGAAGCAATGAAGAAATACAGCCAGATTCTGAGTCACTTTGAAAAGCTG
GAACCTCAGGCAGCAGTTGTGAAGGCTTTGGGGGAACTAGACATTCTTCTGCAATGGATGGAG
GAGACAGAA**TAG**GAGGAAAGTGATGCTGCTGCTAAGAATATTCGAGGTCAAGAGCTCCAGTCT
TCAATACCTGCAGAGGAGGCATGACCCCAAACCACCATCTCTTTACTGTACTAGTCTTGTGCT
GGTCACAGTGTATCTTATTTATGCATTACTTGCTTCCTTGCATGATTGTCTTTATGCATCCCC
AATCTTAATTGAGACCATACTTGTATAAGATTTTTTGTAATATCTTTCTGCTATTGGATATATT
TATTAGTTAATATATTTATTTATTTTTTGCTATTTAATGTATTTATTTTTTTACTTGGACATG
AACTTTAAAAAAATTCACAGATTATATTTATAACCTGACTAGAGCAGGTGATGTATTTTTAT
ACAGTAAAAAAAACCTTGTAATTCTAGAAGAGTGGCTAGGGGGGTATTTCATTTGTAT
TCAACTAAGGACATATTTACTCATGCTGATGCTCTGTGAGATATTTGAAATTGAACCAATGAC
TACTTAGGATGGGTTGTGGAATAAGTTTTGATGTGGAATTGCACATCTACCTTACAATTACTG
ACCATCCCCAGTAGACTCCCCAGTCCCATAATTGTGTATCTTCCAGCCAGGAATCCTACACGG
CCAGCATGTATTTCTACAAATAAAGTTTTCTTTGCATACCAAAAAAAAAAAAAAAAAAAAA

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FIGURE 546

MRQFPKTSFDISPEMSFSIYSLQVPAVPGLTCWALTAEPGWGQNKGATTCATNSHSDSELRPE
IFSSREAWQFFLLLWSPDFRPMKASSLAFSLLSAAFYLLWTPSTGLKTLNLGSCVIATNLQE
IRNGFSEIRGSVQAKDGNIDIRILRRTESLQDTKPANRCCLLRHLLRLYLDRVFKNYQTPDHY
TLRKISSLANSFLLTIKKDLRLSHAHMTCHCGEEAMKKYSQILSHFEKLEPQAAVVKALGELDI
LLQWMEETE

Important features:**Signal peptide:**

amino acids 1-42

cAMP- and cGMP-dependent protein kinase phosphorylation sites.

amino acids 192-195, 225-228

N-myristoylation sites.

amino acids 42-47, 46-51, 136-141

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FIGURE 547

AGCAACTCAAGTTCATCATTGTCCTGAGAGAGAGGAGCAGCGCGGTTCCTCGGCCGGGACAGCA
GAACGCCAGGGGACCCCTCACCTGGGCGCGCCGGGGCACGGGCTTTGATTGTCCTGGGGTCGCG
GAGACCCGCGCGCCTGCCCTGCACGCCGGGCGGCAACCTTTGCAGTCGCGTTGGCTGCTGCGA
TCGGCCGGCGGGTCCCTGCCGAAGGCTCGGCTGCTTCTGTCCACCTCTTACACTTCTTCATTT
ATCGGTGGATCATTTTCGAGAGTCCGTCTTGTAATGTTTGGCACTTTGCTACTTTATTGCTTC
TTTCTGGCGACAGTTCCAGCACTCGCCGAGACCGGCGGAGAAAGGCAGCTGAGCCCGGAGAAG
AGCGAAATATGGGGACCCGGGCTAAAAGCAGACGTCGTCCTTCCCGCCCGCTATTTCTATATT
CAGGCAGTGGATACATCAGGGAATAAATTCACATCTTCTCCAGGCGAAAAGGTCTTCCAGGTG
AAAGTCTCAGCACCAGAGGAGCAATTCAGTAGAGTTGGAGTCCAGGTTTTAGACCGAAAAGAT
GGGTCCTTCATAGTAAGATACAGAATGTATGCAAGCTACAAAAATCTGAAGGTGGAAATTAAA
TTCCAAGGGCAACATGTGGCCAAATCCCATATATTTTAAAAGGGCCGGTTTACCATGAGAAC
TGTGACTGTCCTCTGCAAGATAGTGCAGCCTGGCTACGGGAGATGAACTGCCCTGAAACCATT
GCTCAGATTCAGAGAGATCTGGCACATTTCCCTGCTGTGGATCCAGAAAAGATTGCAGTAGAA
ATCCCAAAAAGATTTGGACAGAGGCAGAGCCTATGTCACTACACCTTAAAGGATAACAAGGTT
TATATCAAGACTCATGGTGAACATGTAGGTTTTAGAATTTTCATGGATGCCATACTACTTTCT
TTGACTAGAAAGGTGAAGATGCCAGATGTGGAGCTCTTTGTTAATTTGGGAGACTGGCCTTTG
GAAAAAAGAAATCCAATTCAAACATCCATCCGATCTTTTCCTGGTGTGGCTCCACAGATTCC
AAGGATATCGTGATGCCTACGTACGATTTGACTGATTCTGTTCTGGAAACCATGGGCCGGGTA
AGTCTGGATATGATGTCCGTGCAAGCTAACACGGGTCCTCCCTGGGAAAGCAAAAATTCCACT
GCCGTCTGGAGAGGGCGAGACAGCCGCAAAGAGAGACTCGAGCTGGTTAAACTCAGTAGAAAA
CACCCAGAACTCATAGACGCTGCTTTCACCAACTTTTTCTTCTTTAAACACGATGAAAACCTG
TATGGTCCCATTGTGAAACATATTTCAATTTTTTGATTTCTTCAAGCATAAGTATCAAATAAAT
ATCGATGGCACTGTAGCAGCTTATCGCCTGCCATATTTGCTAGTTGGTGACAGTGTTGTGCTG
AAGCAGGATTCATCTACTATGAACATTTTTTACAATGAGCTGCAGCCCTGGAAACACTACATT
CCAGTTAAGAGCAACCTGAGCGATCTGCTAGAAAACTTAAATGGGCGAAAGATCACGATGAA
GAGGCCAAAAAGATAGCAAAAGCAGGACAAGAATTTGCAAGAAATAATCTCATGGGCGATGAC
ATATTCTGTTATTATTTCAAACCTTTTCCAGGAATATGCCAATTTACAAGTGAGTGAGCCCCAA
ATCCGAGAGGGCATGAAAAGGGTAGAACCACAGACTGAGGACGACCTCTTCCCTTGTAATTGC
CATAGGAAAAAGACCAAAGATGAACTCTGATATGCAAAATAACTTCTATTAGAATAATGGTGC
TCTGAAGACTCTTCTTAACTAAAAAGAAGAATTTTTTTAAGTATTAATTCATGGACAATATA
AAATCTGTGTGATTGTTTGCAGTATGAAGACACATTTCTACTTATGCAGTATTCTCATGACTG
TACTTTAAAGTACATTTTTTAGAATTTTATAATAAAACCACCTTTATTTTAAAGGAAAAAAA

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FIGURE 548

MFGTLLLYCFFLATVPALAE TGGERQLSPEKSEIWGPGLKADVVL PARYFYIQAVDTSGNKFT
SSPGEKVFQVKVSAPEEQFTRVGVQVLD RKDGSFIVRYRMYASYKNLKVEIKFQGQHVAKSPY
ILKGPVYHENCDCPLQDSAAWLREMNC PETIAQIQRD LAHFPAVDPEKIAVEIPKRFGQRQSL
CHYTLKDNKVYIKTHGEHVGFRI FMDAILLSLTRKVKMPDVELFVN LGDWPLEKKKSNSNIHP
IFSWCGSTDSKDIVMPTYDLTDSVLET MGRVSLDMMSVQANTGPPWESKNSTAVWRGRDSRKE
RLELVKLSRKHP ELIDAAFTNFFFFFKH DENLYGP IVKHISFFDFFKH KYQINIDGTVAAYRLP
YLLVGDSVVLKQDSIYYEHFYNELQPWKHYIPVKS NLSDLLEKLKWAKDHDEEAKKIAKAGQE
FARNNLMGDDIFCYYFKLFQ EYANLQVSEPQIREGMKRVEPQTEDDLFPCTCH RKKTKDEL

Important features:**Signal peptide:**

amino acids 1-17

N-glycosylation sites.

amino acids 302-306, 414-418

cAMP- and cGMP-dependent protein kinase phosphorylation sites.

amino acids 243-247, 495-499

Tyrosine kinase phosphorylation site.

amino acids 341-348

N-myristoylation sites.

amino acids 59-65, 118-124, 184-190, 258-264, 370-376, 439-445

Endoplasmic reticulum targeting sequence.

amino acids 499-504

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FIGURE 549

GGGTGATTGAACTAAACCTTCGCCGCACCGAGTTTGCAGTACGGCCGTCACCCGCACCGCTGC
CTGCTTGCGGTTGGAGAAATCAAGGCCCTACCGGGCCTCCGTAGTCACCTCTCTATAGTGGGC
GTGGCCGAGGCCGGGGTGACCCTGCCGGAGCCTCCGCTGCCAGCGACATGTTCAAGGTAATTC
AGAGGTCCGTGGGGCCAGCCAGCCTGAGCTTGCTCACCTTCAAAGTCTATGCAGCACCAAAAA
AGGACTCACCTCCCAAAAATTCGGTGAAGGTTGATGAGCTTTCACCTACTCAGTTCCCTGAGG
GTCAATCGAAGTATGTGGAGGAGGCAAGGAGCCAGCTTGAAGAAAGCATCTCACAGCTCCGAC
ACTATTGCGAGCCATACACAACCTGGTGTGAGGAAACGTAACCCAACTAAGCCCAAGATGC
AAAGTTTGGTTCAATGGGGGTTAGACAGCTATGACTATCTCCAAAATGCACCTCCTGGATTTT
TTCCGAGACTTGGTGTTATTGGTTTTGCTGGCCTTATTGGACTCCTTTTGGCTAGAGGTTCAA
AAATAAAGAAGCTAGTGTATCCGCCTGGTTTCATGGGATTAGCTGCCTCCCTCTATTATCCAC
AACAAAGCCATCGTGTTTGCCAGGTCAGTGGGGAGAGATTATATGACTGGGGTTTACGAGGAT
ATATAGTCATAGAAGATTTGTGGAAGGAGAACTTTCAAAAGCCAGGAAATGTGAAGAATTCAC
CTGGAACCTAAGTAGAAAACCTCCATGCTCTGCCATCTTAATCAGTTATAGGTAAACATTGGAAA
CTCCATAGAATAAATCAGTATTTCTACAGAAAAATGGCATAGAAGTCAGTATTGAATGTATTA
AATTGGCTTTCTTCTTCAGGAAAACTAGACCAGACCTCTGTTATCTTCTGTGAAATCATCCT
ACAAGCAAACCTAACCTGGAATCCCTTCACCTAGAGATAATGTACAAGCCTTAGAACTCCTCAT
TCTCATGTTGCTATTTATGTACCTAATTAAAACCCAAGTTTAAAAAAAAAAAAAAAAAAAAA
AAAAAAAAAAAAAAAAAAAA

550/550

FIGURE 550

MFKVIQRSVGPASLSLLTFKVYAAPKKDSPPKNSVKVDELSLYSVPEGQSKYVEEARSQLEES
ISQLRHYCEPYTTWCQETYSQTKPKMQSLVQWGLDSYDYLQNAPPGFFPRLGVIGFAGLIGLL
LARGSKIKKLVYPPGFMGLAASLYYPQQAIVFAQVSGERLYDWGLRGYIVIEDLWKENFQKPG
NVKNSPGTK

Important features:**Signal peptide:**

Amino acids 1-23

Transmembrane domain:

Amino acids 111-130

cAMP- and cGMP-dependent protein kinase phosphorylation site:

Amino acids 26-30

Tyrosine kinase phosphorylation site:

Amino acids 36-44

N-myristoylation sites:

Amino acids 124-130;144-150;189-195